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Search information block:
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Query length: 41
Database: EST:*
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Search time (sec): 4390.400000
                          9b_est1:AL659353
9b_est2:BF329967
9b_est2:BF329967
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9b_gss:CNS05D97
9b_est2:BH44947
9b_est2:BH44947
9b_est2:BH44947
9b_est2:BH44947
9b_est2:BH549497
9b_gss:CNS056MU
9b_9ss:CNS056MU
9b_9ss:CNS058M0
9b_gss:CNS0550M0
9b_gss:CNS0550M0
9b_gss:CNS0510P
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gb_est1:AI890775
gb_est1:AU125712
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-Q-/Cgn2_1/USFPO_spool/USO8973363/runat_01082002_080049_18570/app_query.fasta_1.638
-Q-/Cgn2_1/USFPO_spool/USO8973363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST -QEWT=fastap -SUFETX-p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GGAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500 -FEAPOP=6.000
-EALPEXT=7.000 -VGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -VGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pCt -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTEWT=PST -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=USO8973363_@CGN1_1_2938
-NCPU=6 -ICPU=3 -LONGLOC -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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AUTHORS
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                      /organism="Mus musculus"
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7.4e-07
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
Hiramoto,K., Hori,F., Ishil,Y., Ito,M., Kawai,J., Konno,H., Koudo
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
On Jun 29, 2000 this sequence version replaced gi:8811286.
Contact: Yoshihide Hayashizaki
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashira,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB15336 RIKEN full-length enriched, 16 days neonate thymus Mus BB15356 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone Al30024L16 3' sinilar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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ACCESSION
VERSION
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US-08-973-363-6 x BB155356
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 208.00
Ratio: 5.073
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                     AUTHORS
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB461065.2 GI:16426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB461065
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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/clone_lib="RIKEN full-length enriched, 16 days neonate
thymus"
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Identity:
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                                                                                                                                                                       Sasaki
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17

34

489

SOURCE

TITLE

Percent Similarity:

100.000

Percent Identity:

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Gaps:

Quality:

Ratio:

208.00 5.073

KEYWORDS

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alignment_scores:
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jul 21, 2000 this sequence version replaced gi:9356558 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Genome Sequences Mamm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse tissues
                                                                                                                                           was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 130\ {\rm c} 168\ {\rm g} 151\ {\rm t}
                                                                                                                                                                                                                                                                                                              Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, 12 spinal ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
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US-08-973-363-6 x BB461065
FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG 34
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1 (Obases, Totalia, Totalia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P. Shibata,Y. Hayatsu,N. Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected coNas to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-650 (2000)
wagi,K., Fujiwaks,S. Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muzamatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y., Accounty, Muzamatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg MC(B) cDNA Mus musculus cDNA clone G93003JJZ1 3', mRNA
                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sclences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 81-45-503-9222 Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                      ,Y. and Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                       Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Location/Qualifiers
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AUTHORS
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US-08-973-363-6 x BB834922
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VERSION
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LOCUS BB830730
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                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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- 99 c 108 g 100 t
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Length: 41
Gaps: 0
Percent Identity: 95.122

Align seg 1/1 to: BB834922 from: 1 to: 446

BB830730 RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA Mus musculus cDNA clone G930013K04 3', mRNA

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;

Rommalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musidae; Mus.

1 (bases 1 to 438)

1 (bases 1 to 438)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,

Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Y., Tto, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,

Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,

Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,

Matahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., et al.

2001

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci.p., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                              COMMENT
                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est1:AL601246
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                                                                                                       TITLE
                                                                                                                                                AUTHORS
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Ratio:
                                                                                                                                                                                                                                                                                                        430 bp mRNA
DKF2p313J1040_r1 313 (synonym: hlcc2) Homo
DKF2p313J1040 5', mRNA sequence.
AL601246
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                             Bloecker, H.,
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                             Unpublished (1999)
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                           AL601246.1 GI:15164752
                                          Contact: Bloecker
                                                                                  Wiemann,S
                                                                                                     EST (Bloecker, H., Boecher, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki,Y.
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Klopferspitz 18a
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/cell_line="RCB-0527 Jyg-MC(B)"
96 c 108 g 96 t
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4.707
97.619
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  D-82152
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: Identity:
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Martinsried,
                                                                                                       Brandt, P.,
                                                                                                                                           Mewes,W.,
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. 1
. 95.238
Germany
                                                                                                     Mewes, H.W.,
                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                linear EST 14-AUG-2001 sapiens cDNA clone
                                                                                                                                             Weil, B.
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                                                                                                     Weil, B. and
                                                                                                                                           and Wiemann
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ACCESSION
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   Quality:
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US-08-973-363-6 x AL601246
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                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           wm95fl1.x1 NCI_CGAP_Ut2 Homo sapsimilar to SW:CHD1_HUMAN 014646 PROTEIN 1; mRNA sequence.
                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Bmail s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone (DKFZp313J1040) is available at the RZPD in please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI890775
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No s1 sequence available
                                                                                          Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  AI890775.1 GI:5595939
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                 Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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cDNA-collection"
a 81 c 86 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DKF2p313J1040"
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4.579
92.683
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                 Ph.D.,
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LOCUS AU125712
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Ratio: 4.579
Percent Similarity: 92.683
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                                                         Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                    Isogai,T.
HRI human CDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                       Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 866)
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Location/Qualifiers
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Insert Length: 1924 Std Error: 0.00
Seq primer: -40UP from Gibco
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU125712
AU125712.1 GI:10950428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:2443725"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH108"
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US-08-973-363-6 x AU125712
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LOCUS BE895133
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                                                                                                               cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9733 row: h column: 16
High quality sequence stop: 488.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1028)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE895133.1 GI:10358221
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BE895133
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601436690F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921087 5',
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/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NT2RM4"
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/db_xref="taxon:9606"
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/cell_line="NT2"
/note="Vector: pME18SFL3; mR1
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BASE COUNT
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US-08-973-363-6 x BE895133
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LOCUS AL659353
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TITLE
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Ratio:
                                                                                                                                                                                                                                                                     Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus trop!calis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AL659353
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                      119
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."
             /clone_lib="XGC-neurula"
/dev_Stage="neurula"
/lab_host="meurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

134 c 114 g 226 t
                                                                                                                                                                                           /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu045e20"
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4.579
92.683
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Gaps: 1
Percent Identity: 90.244
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tropicalis cDNA clone TNeu045e20 5',
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Library constructed by Life
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JOURNAL COMMENT
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US-08-973-363-6 x AL659353/rev
                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
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 Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est1:AL644594
                                                                                                                                                                                                                                                                                                                                                                         Sequencing primer: PlC This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Silurana.

1 (bases 1 to 645)

Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
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                                        Quality:
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            western clawed frog
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                       Ratio:
                                                                                                                                  a
                                                                                                                          /lab_host="Escherichia coli XL1-blue"
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was oligo dr primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
125 c 156 g 141 t 1 others
172.00
4.649
97.368
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4.649
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Gaps: 0
Percent Identity: 86.842
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alignment_block:

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                                                                                                                                                                                                                                                                                                              BASE COUNT
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                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 AAGCACAAAGACTT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 luAlaGlnArgLeu 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1033 row: k column: 18 High quality sequence stop: 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
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BF239967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/site_3: Sfil (ggccattat
                                                                     147.00
4.455
91.667
                                                                     Percent Identity: 88.889
                                                                                                                                      Length:
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                                                                                                                                  Percent Similarity:
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                                                                                                                                                                   Quality:
Ratio:
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us-08-973-363-6 x CNS04DVG/rev
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LOCUS CNS04DVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 uIleLysLeuLeuSerArgAspLeuAlaLysArgGluAlaGlnArgLeuC 39
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2 (bases 1 to 856)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fisames, C., Wincker, P., Brottier, P., Quetler, F., Saurin, W. and Weissenbach, J.
Sumin, W. and Weissenbach, J.
Sumin, W. and Weissenbach, J.
Sumin, W. and Weissenbach, J.
Unpublished
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Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii, Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 856)
1 (bases 1 to 857)
1 (bases 1 to 858)
1 (bases 1 to 859)
1 (bases 1 to 859)
1 (bases 1 to 859)
1 (bases 1 to 850)
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                                                                                                                                                                                                                                                                                                                                                                                    /Organism="Tetraodon nigroviridis"
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/clone="103K08"
/clone_1ib="c"
/note="Genoscope sequence ID : C0BG103BF04LF1-end : T7"
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                                                                                                                          146.00
4.294
87.179
                                                                                                                          Percent Identity: 74.359
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alignment_scores:
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                               Quality:
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AW996787
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.ludwig.org.br/scripts/gethtml2.pl?t1-&t2-QV3-BN0047-230
200-102-d03&t3-2000-02-23&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
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Location/Qualifiers
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                                                                                                                                                                                                                        /note-"Organ: breast_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
  139.50
4.103
94.444
                                                                                                                                                           low stringency conditions."
59 c 72 g 123 t
                                                                                                                                                                                                      tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="BN0047"
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US-08-973-363-6 x AW996787/rev
       BASE COUNT
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LOCUS AW997058
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                                                                                                                                                                                                                                                                                                                                                                                    Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150 400-152-c03&t3=2000-04-15&t4=1) seq primer: puc 18 forward High quality secures.
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Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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                                                                         /note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under low stringency conditions." 154 \ c \qquad 126 \ g \qquad 241 \ t
                                                                                                                                                                                                           /dev_stage="Adult"
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Ratio: 3.971 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 ATTCTTCCAGATGATCCCGATAA.AAACCACAAGCAAAACAGTTGCAGAC 79
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                                                                                                                                                                                                                                   Genoscope.

Birect Submission

Birect Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more hiformation, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Al352864.1 GI:8246657
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1122)
1 (bases 1 to 1122)
1 Rountenau.L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Meissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO579J 1122 bp DNA linear GSS 26-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
042M09 of library C from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1122)
Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
Ruman gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
Quality: 121.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1122)
                                                                                                                       303 a
                                                                                                              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="042M09"
/clone_Lib="C"
/note="Genoscope sequence ID : COBC042AG05C1-end : T7"
260 c 301 g 246 t 12 others
Length:
29
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alignment_block:
US-08-973-363-6 x CNS05T9J
                                                                                                                                  Ratio: 4.172
Percent Similarity: 100.000
                                                           Align seg 1/1 to: CNS05T9J from: 1 to: 1122
Gaps: 0
Percent Identity: 75.862
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Search information block:
Query: US-08-973-363-7
Query length: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database sequences: 1797656
Database length: 1873333701
Search time (sec): 4907.710000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: Aug 3, 2002 4:26 AM
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08 i A58691 Sequence 10 from Patent
72 i AF004397 Gallus gallus chromo-
3 i A58684 Sequence 3 from Patent W
3 i A58685 Sequence 4 from Patent W
49 i L10410 Mouse DNA-binding prote
1 A58686 Sequence 5 from Patent W
49 i A58686 Sequence 5 from Patent W
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gb_htg:AC101378
gb_ov:CTU89945
gb_pat:AX286188
gb_htg:LMFLCHR36_25
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AUTHORS
TITLE
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ACCESSION
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KEYWORDS
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AUTHORS
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Ratio: 5.000
Percent Similarity: 100.000
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Align seg 1/1 to: A58696 from: 1 to: 1316
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Patent: WO 9639505-A 15 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1. .1316
Other publication AU 5906996 961224 
Location/Qualifiers
                                                                                                                                                                                                                                                                          Sequence 10 from Patent WO9639505.
A58691
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1 (bases 1 to 1316)

Griffiths,R. and Tiwari,B.

AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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                                                                                                        1 (bases 1 to 6608)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                            Patent: WO 9639505-A 10 12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unidentified"
/db_xref="taxon:32644"
493 a 205 c 308 g 304
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Percent Identity: 100.000
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 205.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: A58691
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                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 6872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chicken.
Gallus gallus
                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 800, UK
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/organism="unidentified"
/organism="unidentified"
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SQSGSSDSESGSGSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
LKKQQQQQKAASSDSGSEEDSSSSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGS
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1207 c 1459 g 1
DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
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/db_xref="GI:2501846"
                                                                                                     protein"
                                                                                                                                     /gene="CHD-2"
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain'
/codon_start=1
                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                   /product="chromo-helicase-DNA-binding on the Z chromosome
                                                                                                                                                                                                                          /gene="CHD-Z"
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:2501845
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on the Z chromosome
(CHD-Z) mRNA, complete
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seq_documentation_block:
LOCUS A58684
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US-08-973-363-7 x AF004397
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Sequence 3 from Patent W09639505.
A58684
A58684.1 GI:3714247
                                                 1 (bases 1 to 153)
Griffiths, R. and Tiv
AVIAN GHD GENES AND
                                                                                                                                                                  unidentified
unidentified
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Patent:
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MITHEWMHPOTKRIKENILLTTY EILLKDKSFLGGLWAAPIC IQDITSRU
MITHEWMHPOTKRIKENILLTTY EILLKDKSFLGGLWAAPIC VDEAHRLKNIDSLLY
RTI-IDEKSUHFLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDPEEBIGKGREYGYAS
LHKELEPFLLRKKCWEKSLPAKVEQILRMEMSALQKQYYKWILTRIVKALSKGSKG
STSGFLWIMMELKKCCHHCYLIKPDDWHPQNDLQAQARAHFIGGKKQVNIIYLLVTKGS
GTSGFLWIMMELKKCCHHCYLIKPPDDOMEYWKQEALQHLTRSSGKLILLDHRNAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWHPQNDLQAQARAHFIGGKKQVNIIYLLVTKGS
VEEDILERAKKKMVLDHLVIQRWDTTGKTVLHFGSTPSSTSTPFWKEELSAILKFGAEE
LFKEPEGEEQEPQEMDIDE ILKRAETRENEEPGPLYGDELLSQFKVANFSNMDEDDIE
LEPERNSRNWEELI PESGRRT LEEEEROKELEEIYMLPHARCAGISFWGSEGRRS
SRRYSGSDSGTTERKRPKKRGRPRTIP RENIKGFSDABILKFTASKYKKGGFLERL
AVARDAELVDKSETDLRRLGGLYHNGCI KALKDNSSGQERAGGRLGKVKGPTFRISGV
QVNAKLVISHEEELAPLHKSI FSDFEERRRYVIFCHTKAAHFDLIMGKEDDSNLLVGI
YEXGYGSWEMIKMDPDLSLTQKILLDDDPKRPQAKGLGFRADFLLKGLARKCDEVKYK
HLHKKIKTEKBWEEKPEDIGIKKEAEERRETKEKENKELKREKEKENKELKEKD
NEKREMKYKESTOKEKENKEEKKENKELKEERDLHTTGCL
KEYTNPGGIKOWRKULMIFVSKSTEFDARKLHKLYKHAIKKRGESGQHUDONISSWVN
THVIRNPDVERLKETTHBDDSSRDSYSSDRHLSGYHDHKRHGROTKKSDSYKKSDSKRRAPY
TAPSTRUKTONISSWVN
WO 9639505-A 3 12-DEC-1996;
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AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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1223 c 1520 g
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                                                 Tiwari, B.
AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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Percent Identity:
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100.000
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BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE

JOURNAL

SOURCE ORGANISM

ACCESSION VERSION

DEFINITION

4180

KEYWORDS

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REFERENCE
AUTHORS
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FEATURES
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US-08-973-363-7 x A58684
                                                                                                                                                alignment_block:
US-08-973-363-7 x A58685
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                                                                                                                                                                                                                                                             Quality: 190.00
Ratio: 4.634
Percent Similarity: 80.392
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Ratio: 4.634
Percent Similarity: 80.392
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                                                                            Align seg 1/1 to: A58685 from: 1 to: 153
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1 (bases 1 to 153)

1 (bases 1 to 153)

Griffiths, R. and Tiwari, B.

AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Other publication AU 5906996 961224.
Location/Qualifiers
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40 c 31 g 24
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Percent Identity: 80.392
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Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center,
7701 Burholme Avenue, Philadelphia, PA 19111, USA
On Feb 16, 1994 this sequence version replaced gi:293322.
Location/Qualifiers
1. 5349
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Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWIZ-1; lke helicase domain
SNF2/SWIZ-1; lke helicase domain
Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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YKTILDFKSNHRLLITGTPLONSIKELMSLIMER MERKESSMEDFEERENGKRERYGYA
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ELFKERDEGESEPOEMDIDELIKRAFTHENEFGFLSVGDELLSGFKVANESNMDEDDI
ELFERRINSKNWEBITPEDENKRGFRFTITPRBNIKGFSDAEIRRYKRFGGPDLERL
BLEFERNSKNWEBITPEDGRRKKRGFFTITPRBNIKGFSDAEIRRYKKFGGPTENSK
SRSHRYSGSBOSSISBEKRFKKRGFFTITPRBNIKGFSDAEIRRYKKFGGPDLERL
DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSSGTERAGGRILGKYKGFTFRISG
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IAHSNQKSAAGLPDYYCKMQGLPYSECSWEDGALISKKFQTCIDEYFSRNQSKTTPFK
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GKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSMQREIQTWASQMNAVVYLGDINSR
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DCRVGRKGATGATTI I YAVEADGDPNAGFERNKEPGD I QYLI KWKGWSHI HNTWET EE
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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IYEYGYGSWEMIKMDEDLSLTHKILPDDPDKKPQAKQLQTRADYLKKLLSRDLAKREA
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DRSKKSYVSDAPVHIPASGEEPVPLAEBSEELDQKTFSICKEENRPVKAALKQLDRPEK
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HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT"
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LOCUS AF006513
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US-08-973-363-7 x A58683
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Sequence 2 from Patent W09639505
A58683
         \begin{array}{ll} \text{Homo sapiens CHD1 mRNA,} \\ \text{AF006513} \end{array}
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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AF006513.1 GI:2645428
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1 (bases 1 to 5947)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hietter, P. and Collins, F.S. Characterization of the CHD family of proteins

Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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t Drive, Bethesda, MD 20892-4442,
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KUXKHAIKKROESQONSDQNSULAPHVIKNPEQIKOWRKNIKMIYOSSKESSESBRLITO
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RASSGERSFENDQRSYGSRSPEBHSVEHKSTPEHTWSSRKT"

1004 c 1243 9 1570 t
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KGSVEEDILERAKKKWLDHLYIQRADJTTGKTVLHTGSAPSSSTPPKEELSAILKEG
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REGERVLIFSOWVEMLDILAFYLKYRGFFPGLLOGSIKGELRKQALDHFNAEGSE
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EETLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVETYNCQOELTDDLHKQYQIVG
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FKDCKVLKQRPRFVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEM
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DDDEEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEEEEFETIER
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KKQQQQQQQQQHQASSNSGSEEDSSSSEDSDDSSSEVKRKKHKDEDWQMSGSGSPSQS
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                                                                                      Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
                                                                                                                                                                                                     Percent Similarity:
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26932 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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                        1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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[ [bases ] to 101220)
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                            rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
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                                                                                                                                                                               ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC
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                                   AAGCT.....CTTTCTGGTGCG 118363
                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
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Submitted (31-OCT 1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mi
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-JUN-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 134365)
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DOE Joint Genome Institute.
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4.359
95.122
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/db_xref="taxon:9606"
/chromosome="5"
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Percent Identity:
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ne 5 clone CTD-2082I17, complete sequence.
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AUTHORS
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ORGANISM
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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TITLE
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seq_documentation_block:
LOCUS AC021449
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                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zimmer, A. and Zody, M. Direct Submission
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AC021449.3 GI:10047806
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Sequenciny vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                          as soon as it is available and the accession number will be preserved.
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Contact: sequence_submissions@genome.wi.mit.edu
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3820: contig of 38820 bp in length
38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511: gap of 100 bp
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seq_name: gb_htg:AC008531
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US-08-973-363-7 x AC021449
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ORIGIN
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Percent Similarity:
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                                                                  116247 AAGCT.....CTTTCTGGTGCG 116263
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43380 43379: gap of
45905: contig of 3528 bp in length
46906 47005; gap of
47006 51830: contig of 4825 bp in length
51831 51930: gap of
51931 62619: contig of 1689 bp in length
65270 75408: contig of 1689 bp in length
62720 75408: contig of 12689 bp in length
75409 75508: gap of
75509 92516: contig of 100 bp
75509 92516: contig of 100 bp
75509 106400 is contig of 1700 bp in length
106410 106509: gap of
106509: gap of
106410 106509: gap of

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43971 a 26246 c 26678 g 45278 t
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4.359
95.122
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clone_end:T7
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clone_end:SP6
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/db_xref="taxon:9606"
/clone="RP1-58M12"
/clone_1ib="RPCI-11 Human Male BAC"
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38921. .40411
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92617. .106409
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75509..92516
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51931. .62619
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17006. .51830
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43380. .46905
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10512. .43279
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Gaps: 1
Percent Identity: 85.366
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REFERENCE
AUTHORS
TITLE
                                  alignment_scores:
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LOCUS AC008531
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 14274 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145659 bp DNA linear HTG 14-FEB-2001
Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
7 ordered pieces.
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Center clone name: CIT-HSPC_480Bl1
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Center: Joint Genome Institute
Center Code: JGI
Quality:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14559)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                     /chromosome="5"
/clone="CTC-480B11"
/clone_lib="CalTech human BAC library C"
/clone_lib="CalTech human BAC library C"
/clone_lib="CalTech human BAC library C"
    170.00
                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location
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    41
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
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Percent Similarity:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                            Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 5 clone RP PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing of Human Chromosome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 193446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                            Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                        Center clone name: RPCI-11_360I2
                                                                                                                                                                                                                                                                                                                                                                                         Center Project Name: 544799
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.jgi.doe.gov
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1459
2668
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3824
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95.122
1358: contig of 1358 bp in length
1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
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Percent Identity: 85.366
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me 5 clone RP11-36012, *** SEQUENCING IN
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                                  alignment_scores:
                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                               FEATURES
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   Quality:
Ratio:
                                                                                                  57571
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1110867
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1123739
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102795
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16482
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9197
10261
10361
12461
12561
14612
14712
                                                                                                                                             /organism="Homo sapiens"
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/chromosome="5"
                                                                                             /clone="RP11-36012"
/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
                                                                                                                                                                                                            Location/Qualifiers
   170.00
4.359
                                                                                                                                                                                                                                                                       92891: gap of unknown length
102794: contig of 9903 bp in ler
102894: gap of unknown length
110866: contig of 7972 bp in ler
110966: gap of unknown length
117571: contig of 6605 bp in ler
117671: gap of unknown length
1123738: contig of 6067 bp in ler
1123738: contig of 6067 bp in ler
123838: gap of unknown length
130833: contig of 6745 bp in ler
130838: gap of unknown length
141544: contig of 10861 bp in le
141644: gap of unknown length
141544: gap of unknown length
                                                                                                                                                                                               .193446
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169209: gap of unknown 1
193446: contig of 24237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown contig of 5180
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contig of 6151 bp in
gap of unknown length
contig of 5563 bp in
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g of 3324
f unknown
g of 4978
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g of 1670
f unknown
g of 1487
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g of 7616
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of 5982
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g of 4585
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y of 2366
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of 1474
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   Length:
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percent Identity: 85.366

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alignment_block:
US-08-973-363-7 x AC091946
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GI:14277282

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 95.122
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    Quality:
    Ratio:
    Percent Similarity:
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source
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US-08-973-363-7 x AC026778/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished

CE (bases 1 to 19543)

CE (bases 1 to 19543)

CE (bases 1 to 19543)

RE DOE Joint Genome Institute.

RISDIRECT Submission

AL Submitted (24-MAR-2000) production Sequencing Facility, DOE Joint Genome Institute, 2800 witchell Drive, Walnut Creek, CA 94598, USA

CE (cenome Institute, 2800 witchell Drive, Walnut Creek, CA 94598, USA

CE (cenome Institute and Stanford Human Genome Center.

RS DOE Joint Genome Institute and Stanford Human Genome Center.

RS DOE Joint Genome Institute and Stanford Human Genome Center.

RS DOE Joint Genome Institute and Stanford Human Genome Institute, 2800 Mitchell birty, Walnut Creek, CA 94598, USA

On Jun 1, 2001 this sequence version replaced gi:13677045.

Draft Sequence Produced by DOE Joint Genome Institute

WWW.jgl.doe.gov

WWW.jgl.
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9806"
/chromosome="5"
/chome="CTC-428111"
/clone="CTC-428111"
/37302 c 37040 g 58329 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .195433
                                                                                                                                                            170.00
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                                                                                                                                                            Length: 41
Gaps: 1
Percent Identity: 85.366
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Align seg 1/1 to reverse of: AC026778 from: 1 to: 195433
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Search information block:
Query: US-08-973-363-7
Query length: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.62000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: Aug 3, 2002 4:34 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
-MODEL=frame+_p2n.model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of: US-08-973-363-7 to: N_Geneseq_032802:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           time (sec): 523.620000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _p2n.model -DEV-xlh
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            alignment_scores:
                             1188 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
                                                17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
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seq_documentation_block:
ID AAT42754 standard; cD
XX AAT42754;
AC AAT42754;
XX 12-MAR-1997 (first e
DT 12-MAR-1997 (first e
DT 12-MAR-1997 (first e
DT 12-MAR-1997 (first e
DT 12-DEC-1996;
XX 6allus sp.
XX W09639505-Al.
XX W09639505-Al.
XX 06-JUN-1996; 956WO-G
PF 05-JUN-1996; 956WO-G
XX (1SIS-) ISIS INNOVATI
XX (1SIS-) ISIS INNOVATI
XX U15HITS R, Tiwari
XX Claim 1; Fig 8; 76pp;
XX The chicken CHD-W gen
CC The chicken 
                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-973-363-7 x AAT42754
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/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF90032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 205.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                              Align seg 1/1 to: AAT42754 from: 1 to: 1316
The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHB-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a relation to the sex of progeny of the sex of the sex of the sex of progeny of the sex of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird; sex determination; chromodomain-Helicase-DNA binding 1 avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 8; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken CHD-W gene (partial sequence).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 41
Gaps: 0
Percent Identity: 100.000
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luAlaGlnArgLeuAlaGlyAla 41

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alignment_block:
                                                                                                                                                                                                                                                                               alignment_scores:
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ID AAT42751 standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1997.DAT:AAT42751
                                                                                         Align seg 1/1
                                                                                                                                          US-08-973-363-7 x AAT42751
                                                                                                                                                                                                              Percent Similarity: 100.000
4080 ATTTTACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                       The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken CHD-1A gene
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                                                                                                                                                                                                                                                                                                                                                     Sequence 6608 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS
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                        1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex determination; chromodomain-Helicase-DNA binding
; chromodomain-Helicase-DNA binding on the W chromoson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                        Ratio:
                                                                                            to: AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-GB01341
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228..5390
/*tag= a
                                                                                                                                                                                                                                      205.00
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                                                                                                                                                                                                                                                                                                                                                     A;
                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                     1207 C;
                                                                                                                                                                                                              Percent
                                                                                                                                                                                                           Length:
Gaps:
t Identity:
                                                                                            to: 6608
                                                                                                                                                                                                                                                                                                                                                     1459 G; 1653 T; 0 other;
                                                                                                                                                                                                           : 41
: 0
: 100.000
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  4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Avian;
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17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG

34

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seq_documentation_block:
ID AAT42757 standard; DN
XX
AC AAT42757;
XX
Chick CHD-1A gene fra
XX
Bird; sex determinat;
KW Bird; sex determinat;
KW CHD-1A; CHD-W; W chrc
XX
Gallus sp.
Ytag
FT misc_difference 52..6
FT misc_difference 52..6
FT pN W09639505-A1.
XX
PN W09639505-A1.
XX
12-DEC-1996.
Y*tag
FT
XX
PN W09639505-A1.
XX
C12-DEC-1996.
Y*Tag
FT
XX
PN W09639505-A1.
XX
C12-DEC-1996.
XX
PN W09639505-A1.
XX
C12-DEC-1996.
Y*Tag
FT
XX
PN W09639505-A1.
XX
C12-DEC-1996.
Y*Tag
FT
XX
PN W09639505-A1.
XX
PN W09639505-A1.
XX
C12-DEC-1996.
Y*Tag
FT
XX
C1-DEC-1996.
XX
PP
C1-DEC-1996.
XX
C1-1997-043127/04.
XX
PP
C1-18 Sec also AAT7
CC Cacid sequences of the cl
CC CHD-1A (see also AAT6
CC cembryo, foetus etc..6
XX
SQ Sequence 153 BP; 58 J
                                                                  alignment_block:
US-08-973-363-7 x AAT42757
                                                                                                                                                           alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name:
                                 Align seg 1/1 to:
                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding CHD-lA; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chick CHD-1A gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
l IleLeuProAspAspProAsp......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                            Ratio:
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                                   AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95GB-0011439
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and are ignored in a
acid sequence given
                                                                                                                        190.00
4.634
80.392
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                                                                                                                                                                                                                                  A;
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                                     from:
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                                                                                                                        Length:
Gaps:
Percent Identity:
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                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                  G;
                                     ç
ö
                                                                                                                                                                                                                                  24 T; 0 other;
                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a repeat of bases in the translated iven in Fig 3"
                                                                                                                        51
1
80.392
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seq_documentation_block:
ID AAT42758 standard; DNA; 153 BP
                       alignment_scores:
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                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42751) and chD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                           Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                    Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chick CHD-W gene fragment.
                                                                Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT42758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                                                                                                                                                                                                                            1997-043127/04.
DB; AAW08148.
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHD-W; W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                    Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                        95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                   96WO-GB01341
190.00
4.634
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                                                             56 A; 36 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS.
                                                                31 G;
                                                              30 T; 0 other;
 51
1
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1 amino
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seq_documentation_block:
ID AAT42759 standard; DNA; 153 BP
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US-08-973-363-7 x AAT42758
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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW84164-49. The CHD-IA (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                        Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                     Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 CAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATTTTACCTGATGATCCAGATAAGAAACCCCCAGGCTAAGCAGTTACAGAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IleLeuProAspAspProAsp...... 7
                                                                                                                                                                                                                                                                                                                                                                                                                1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                     AAW08149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB01341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
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amino
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foetus etc. and

to manipulate the

sex of progeny.

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alignment_block:
US-08-973-363-7 x AAT42759
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                                                                                                                                                                                                                                                                                                                                                      ID AAT42756 standard;
                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                   151
 Claim
                                              WPI; 1997-043127/04.
P-PSDB; AAW08146.
                                                                        Griffiths R,
                                                                                                             06-JUN-1995;
                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                    Mus sp
                                                                                                                                                                                                                                                                      CHD-1;
                                                                                                                                                                                                                                                                                                                   12-MAR-1997
                                                                                                                                                                                                                                                                                                                                      AAT42756;
                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AATTACTGAATAAAGACCTTGCAAGAAAAGAAGTGCAAAGACTTACTGGT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 153
                 Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                           (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                 12-DEC-1996
                                                                                                                                                                   WO9639505-A1
                                                                                                                                                                                                                                                                                                 Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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                                                                                                                                                                                                                                                                                                                                                                                                   GCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                      Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                               ysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleLeuProAspAspProAsp.....
 8
                                                                                                                                                                                                                                                                    CHD-W; W chromosome; ss.
Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                         Tiwari B;
                                                                                                             95GB-0011439
                                                                                                                               96WO-GB01341
                                                                                                                                                                                                                       Location/Qualifiers 52..81
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4.439
80.392
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                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;
                                                                                                                                                                                   "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
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                                                                                                                                                                                                                                                                                                                                                       153
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0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u> 51
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                                                                                                                                                                                              22-51
amino
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*88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-973-363-7 x AAT42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAT42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT44757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW408146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAW42754-55) genes determine sex in birds and can be used to identify AAW42754-55) genes determine sex in birds and can be used to identify
                                                                                                                                                                                                                                                                                                                                                        Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 GCG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                          ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AACTACTTAGCAGAGATCTTGCAAAAAGAGAGGCTCAGAGACTTTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 ysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 CAAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IleLeuProAspAspProAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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                                                                                                                                                                                                                      Location/Qualifiers
1..1311
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4.195
80.392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                           telangeictasia; Down's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
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                                                                                                                                                                                                                                                                                                              viral.
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seq_documentation_block:
ID AAK88882 standard; cDNA; 4;
XX
AC AAK88882;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system anti
XX
Human; digestive system anti
XX
KW Human; digestive system anti
XX
KW digestive system disorder;
XX
KW digestive system disorder;
XX
DE Homo sapiens.
XX
PN W0200155314-A2.
XX
PN W0200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001W0-US01324
XX
PF 17-JAN-2000; 2000US-0180628
PR 04-FEB-2000; 2000US-0186362
PR 04-FEB-2000; 2000US-0184664
PR 16-MAR-2000; 2000US-0188974
E Land
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality: 129.00
Ratio: 5.160
Percent Similarity: 100.000
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US-08-973-363-7 x AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK88882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                        31-JAN-2000; 2000US-0179065, 04-FEB-2000; 2000US-0130628. 24-FEB-2000; 2000US-0184664. 02-MAR-2000; 2000US-0186350. 16-MAR-2000; 2000US-0189874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                17-JAN-2001; 2001WO-US01324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-480769/41.
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Gaps: 0
Percent Identity: 100,000
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26-JUL-2000

26-JUL-2000

14-AUG-2000

12-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

23-AUG-2000

24-AUG-2000

25-SEP-2000

26-SEP-2000

27-SEP-2000

28-SEP-2000

28-SEP-2000

29-SEP-2000

14-SEP-2000

14-SE
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18-APR-2000;
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2000US-020515.
2000US-020515.
2000US-02014886.
2000US-0211135.
2000US-0211880.
2000US-0211890.
2000US-02118290.
2000US-02118290.
2000US-021954.
2000US-022953.
2000US-022953.
2000US-0225213.
2000US-0225213.
2000US-0225213.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225275.
2000US-0225758.
2000US-0225758.
2000US-0225758.
2000US-0225758.
2000US-0225758.
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17-NOV-2000
01-DEC-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
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20-OCT-2000
20-OCT-2000
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20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
01-NOV-2000
08-NOV-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                              Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders o digestive system, particularly cancer and cancer metastases - \frac{1}{2}
                                                                                                  WPI; 2001-502630/55
P-PSDB; AAM93109
                          Claim
                                                                                                                                              Rosen
                          <u>,</u>
                                                                                                                                             CA,
                                                                                                                                                                       HUMAN
                          SEQ
                                                                                                                                            Barash SC,
                                                                                                                                                                                              2000US-0239937

2000US-0241785

2000US-0241786

2000US-0241808

2000US-0241808

2000US-0244617

2000US-0246474

2000US-0246475

2000US-0246478

2000US-0246478

2000US-0246524

2000US-0246524

2000US-0246523

2000US-0246523

2000US-0246523

2000US-0246528

2000US-0246528

2000US-0246611

2000US-0246611

2000US-0246611

2000US-0246611

2000US-0249218

2000US-0251868

2000US-0251868

2000US-0251868

2000US-0251989

2000US-0251999

2000US-0251999

2000US-0251999

2000US-0251999

2000US-0251999
                          IJ
                                                                                                                                                                       GENOME
                        NO 1198;
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                                                                                                                                             Ruben
                     986pp;
                                                                                                                                             M.
                        English.
                                                               of
                                                                the
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The present invention provides the protein and coding sequences

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SSSSSSXX
                                                                                                                                                                                                                                                                                                                                                                                 seq_name:
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US-08-973-363-7 x AAK88882
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                             Human; colorectal cancer; colorectal cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 421 BP;
                                                                                                                                                                                                                                                                                                                                                                                                    210 GGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CCGAGCGGATTACTTGTTGAAGCTGCTCAGAAAGGGTCTGGAGAAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                     34 luAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI57603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                    214
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 2000US-0184664.
2000US-0189874.
2000US-0199076.
2000US-0199076.
2000US-029515.
2000US-0299467.
2000US-0214886.
2000US-0215647.
2000US-0216647.
2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
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2000US-0180628
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                                                                                                                                                                                                                                                                                               cancer antigen cDNA
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4.067
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 A;
                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                                                                                                 entry)
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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71.429
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                                                                                                                                                                                                                                                                            gene therapy; ss
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2000US-0225213 2000US-0225214

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17-NOV-2000
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17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000
                                                   The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in the AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-457727/49.
P-PSDB; AAM38625.
Sequence 421 BP; 148 A;
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0246523

2000US-0246524

2000US-0246526

2000US-0246532

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2000US-0249207

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2000US-0249213

2000US-0249213

2000US-0249214

2000US-0249214

2000US-0249216

2000US-0251931

2000US-0251931

2000US-02511868

2000US-02511868

2000US-02511869

2000US-02511869
78 C;
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61 T; 7
other;
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2000US-022924 2000US-0229243 2000US-0229343 2000US-0229345 2000US-0229513 2000US-023943 2000US-023943 2000US-0231244 2000US-0231244 2000US-0231244 2000US-0231241 2000US-0231241 2000US-0231261 2000US-0231263 2000US-0231263

14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-OCT-2000;
02-OCT-2000;
03-OCT-2000;
03-OCT-2000;
04-OCT-2000;
05-OCT-2000;
06-NOV-2000;
08-NOV-2000;

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alignment_scores:
 Quality:
 Ratio:

122.00 4.067

Length: Gaps:

35

alignment_block: US-08-973-363-7 x ABL06443

Percent Similarity:

Quality:

Ratio

88.00 2.839 81.579

Percent Identity:

55.

Length: Gaps:

Align seg 1/1 to:

ABL06443

from:

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to: 6240

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seq_documentation_block:
ID ABL06443 standard;
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL06443
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                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                    Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English
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                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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11-JUL-2000; 2000US-0614150
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alignment_scores

Sequence 6240 BP;

1675

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1682

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1760 G; 1123

H.

Sequence

9933

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2468 C;

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The sequence data for this patent did not form specification, but was obtained in electronic i

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of the printed t directly from

WIPO

ftp.wipo.int/pub/published_pct_sequences

(ABB57737-ABB72072)

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seq_documentation_block:
ID ABL06442 standard;
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                                                               useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                       The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                         Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and
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P-PSDB; ABB62339.
                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                   capable
                                                                                                                                                               The invention relates to an isolated nucleic acid detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 85; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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, Carter D;
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seq_documentation_block:
ID AAS96071 standard; cD
XX AAS96071;
XX AAS96071;
XX AC AAS96071;
XX 26-FEB-2002 (first e
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leishmaniasis; Leishmania antigen; immunostimulant; protozoacide; Ldp23; interleukin-15; PCR primer; Lbhsp83; ML5; Lt-1; LbeIF4A; Lmsp1a; Lmsp9a; MAPS-1A; Lmg5P1; Lmg5P3; Lmg5P5; Lmg5P8; Lmg5P9; Lmg5P1; Lsq5P19; ss; Lcq5P1; Lcq5P1
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                                                                                                                                                                                                                                                                                                                                                                              05-APR-2001; 2001WO-US11254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania antigen 4G2-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ProAspAspProAspLysLysProGlnAlaLysGln....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGAGACGTGTAGCGGGA 7414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luAlaGlnArgLeuAlaGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCATCGAGCGCGTACTCGACGATCGTCCGAAAAGATGTTTCCCGTAGCA 7394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/hold-geneseq/geneseqn~embl/NA2002.DAT:AAS96071
                                                                       Campos-Neto
Probst P;
                                                                                                                                                                                                                                      ; 2000US-0551974.
; 2000US-0565501.
; 2000US-0639206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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2.103
72.500
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                                                                                                           Webb
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Gaps:
Percent Identity:
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                                                                                                           JR,
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                                                                                                           Dillon DC,
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Skeiky YAW,

Bhatia

New isolated Leishmania antigens, useful for prevention, to diagnosis of leishmaniasis, also related nucleic acids for

treatment or genetic

and

Example 2; Fig 1; 87pp; English

AAU71861

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seq_documentation_block:
ID AAZ30163 standard; DN
XX
AC AAZ30163;
XX
DT 26-JAN-2000 (first 6
XX
Complete nucleotide 8
XX
PAV-3; defective recomplete standard; pn
KW PAV-3; defective recomplete standard; pn
KW genetic disease; hemo
KW genetic disease; hemo
KW genetic disease; hemo
KW acquired immune defic
XX
POPTCINE adenovirus T;
XX
W09953047-A2.
XX
W09953047-A2.
XX
YX
PD 21-OCT-1999.
PD 21-OCT-1999.
PD 21-OCT-1999; 99WO-10
XX
PD 21-OCT-1999; 99WO-10
XX
ROSS PORTINO SKATCI
XX
READY PS, Tikoo SK,
XX
PA (UYSA-) UNIV SASKATCI
XX
NO WPI; 1999-620422/53.
XX
NO New nucleic acids fro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polypeptides comprising an immunogenic part of Leishmania antigen. The Leishmania polypeptides and their associated DN sequences, epitopes and fusion proteins are used in the production of compositions used for inducing a protective immune response against leishmaniasis, for prevention and treatment of the disease. The compositions can also be used generally to treat diseases that respond interleukin-15 stimulation. In addition, the products may contain an immunostimulant. The sequences represent cDNA molecules encoding Leishmania antigens and PCR primers used to amplify DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                       subunit vaccine; nucleic acid immunisation; gene therapy; genetic disease; hemophilia; cystic fibrosis; cancer; viral infection acquired immune deficiency syndrome; PAV antigen; porcine pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352
New nucleic acids from the genome of porcine adenovirus-3, gene therapy vectors, particularly for immunization -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccination
                                                             WPI; 1999-620422/53
                                                                                                                                                                                                                                                                                                                                                                                                                                       PAV-3; defective recombinant PAV vector; live recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1908
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                                                                                                  Tikoo SK,
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                                                                                                                                        SASKATCHEWAN
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                                                                                                                                                                               98US-0081882
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3.529
89.474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193pp; English.
                                                                                                  Babiuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34094 BP
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                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the PAV-3
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0
52.632
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viral infection;
-^+hoden; ds
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                      and derived
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polynucleotides sequences are used to produce (recombinant or defective) vectors that can express heterologous proteins, e.g. for making live, recombinant virus or subunit vaccines, for nucleic acid immunisation or for gene therapy (e.g. of genetic diseases such as hemophilia or cystic fibrosis, cancer, or viral infections, including acquired immune deficiency syndrome), also for in vitro expression of recombinant antigens (for antibody production), antisense RNA, ribozymes or therapeutic proteins. They are also used diagnostically to detect PAV antigens and/or nucleic acid. The vectors may be used in human or veterinary medicine, but particularly for expressing protective determinants of porcine pathogens. Regulatory regions may be used to control expression of heterologous genes. Antibodies raised against PAV-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a defective recombinant PAV vector comprising inverted terminal repeats (ITR), packaging sequences and at least one heterologous nucleotide sequence (II), but lacking El functions. The defective vectors replicate inefficiently in cells (other than helper cells) so are unlikely to be immunogenic. Deletion of the El (and optionally other regions) increases the size of heterologous insert that can be packaged. The PAV-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the complete nucleotide sequence of the genome of porcine adenovirus-3 (PAV-3). The specification also describes
     Sequence 34094
                                                                                                                                                                 polypeptides can also be used
     BP;
     6240 A;
11070 C; 10693 G; 6091 T; 0 other;
                                                                                                                                                                 for diagnosis (to detect PAV-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also describes
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seq_documentation_block:
ID AAX39679 standard; DN
XX
AC AAX39679;
XX
Cancer associated ant
XX
Cancer associated ant
XX
KW Cancer associated cancer; colon
KW prostate cancer; ss.
OS Homo sapiens.
XX
PN WO9904265-A2.
XX
PD 28-JAN-1999.
XX
XX
XX
Z2-JUN-1997;
Z2-JUN-1997;
Z3-JUS-1997;
Z3-JUS-1
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US-08-973-363-7 x AAZ30163/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renal cancer associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 rLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:AAX39679
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    98US-0102322.
97US-0896164.
97US-0061599.
                                                                                                                                                                    98WO-US14679
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2.786
65.625
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cancer;

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alignment_scores: 57.50
Quality: 57.50
Ratio: 2.130
Percent Similarity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-973-363-7 x AAX39679
                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAX39679 from: 1 to: 2911
                                                                                                                                                                                                                                                    10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                               1761 GTTTGAGAACCTCTGCAAAATCATG...AAAGACATATTGGAGAAAAAG 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen precursors expressed in human breast which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and ling cancer.
1808 TGAAAAGG 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2911 BP; 957 A; 519 C; 686 G; 749 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 67; Page 496-497; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-132448/11.
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Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E;
Tureci O;
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                                                        35 laGlnArg 37
                                                                                                                                                                     97US-0061765.
97US-0948705.
97GB-0021697.
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Gaps: 1
Percent Identity: 30.556
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9b_gss: CNSO54WU
9b_gss: CNSO56WU
9b_gss: CNSO2BFS
9b_gss: CNSO2BFS
9b_gss: CNSO2SWU
9b_gss: CNSO2SWU
9b_gss: CNSO3SWU
9b_gss: CNSO5SWU
9b_gss: CNSO5WU
9b_gss: CNSO
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9b_est1:AB83773
9b_est1:AG01246
9b_est1:AG90775
9b_est1:AH290775
9b_est2:BB95133
9b_gss:CNS04DVC
9b_est2:BR339677
9b_est1:AW996787
9b_est1:AW99703
9b_gss:CNS05797
9b_est1:AW9703
9b_gss:CNS05797
9b_est1:AA305793
9b_est1:AA305793
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gb_est1:BB155356
gb_est1:AL644594
gb_est1:BB461065
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Database length: -1841457050
Search time (sec): 4390.400000
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Query: US-08-973-363-7
Query length: 41
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-Q-/cgn2_1/USEPG_spool/USG8973363/runat_01082002_080049_18570/app_query.fasta_1.638
-Q-/cgn2_1/USEPG_spool/USG8973363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST_-OFM-fasta_ SUFFIX-P2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH-0.100 -LOOPCL-0.000 -NOOPEXT=0.000 -QGAPOP=4.500
-GGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -EELOP=6.000
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gb_est2:BM070535
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gb_est2:BM185005
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                                         seq_name: gb_est1:BB155356
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alignment_block:
US-08-973-363-7 x AL659353/rev
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                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AL659353 from: 1 to: 593
                                                                                                                                                                              246 AAGCACAAAGACTTTCT 230
                                                                                     296 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG
                                     34 luAlaGlnArgLeuAla 39
                                                                                                           17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
                                                                                                                                                                                                1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinxton, Cambridgeshire, CBIO 15A, UN Email: tropEsanger.ac.uk
Sanger Xenopus tropLcalis EST project 2001
TROPICALIS_SQUENCE_ID: TNeu045e20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 593)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus troploalis BST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL659353 XGC-neurula Silurana tropicalis cDNA clone TNeu045e20 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AL659353
AL659353.1 GI:17672995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             western clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="TyNeu045e20"
/clone="TyNeu045e20"
/clone_11b="XGC-neurula"
/dev_stage="neurula"
/lab_host="Rescherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/notc="Pector: pCS107; Site_1: EcoRI; Site_2: NotI: cDNA
was oligo dT primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
a 134 c 114 g 226 t
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/db_xref="taxon:8364"
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                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB155356 RIKEN full-length enriched, 16 days neonate thymu musculus cDNA clone Al30024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp/further details.
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDMAs to
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Email: genome-res@qs
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Tel: 81-45-503-9222
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

Unpublished (2001)

On Jun 29, 2000 this sequence version replaced gi:8811286.

Contact: Yoshihide Hayashizaki
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Arakawa,T., Carninci,P., Fukuda,S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BB155356.2 GI:16268254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with luman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                          /tissue_type="thymus"
/dev_stage="16 days ne
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                          /clone="A130024L16"
                                                                   /lab_host="DH10B"
                                                                                             days neonate"
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                                                                                                                                                                                                                                                                                                                                                                                                           Riken contributed to
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thymus Mus
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AUTHORS
TITLE
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ORGANISM
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us-08-973-363-7 x BB155356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGCTCAGAGACTTTGTGGTGCG 611
                                                                                                                                                                                     Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
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                                                         Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL644594 XGC-egg Silurana tropicalis cDNA clone L1E1d12
                                                                                                                                                                        Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                          Silurana tropicalis
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  constructed by Aaron M.
                                       Sequencing primer: P1C
                                                                                                                              Hinxton, Cambridgeshire,
                                                                                                                                                  Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                    western clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
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                        sequence is from a Xenopus
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a 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN. Division of Experimental Animal Research in Rik
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Gaps:
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                        Gene Collection (XGC) library
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in Riken
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/db_xref="taxon:8364" /clone="L1E1d12"

organism="Silurana tropicalis"

Location/Qualifiers

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REFERENCE
AUTHORS
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US-08-973-363-7 x AL644594
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LOCUS BB461065
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Fax: 81-45-503-9216
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-rapper-selected cDNAs to
prepare full-length cDNA libraries for rapper discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB461065 660 bp mRNA linear EST 25-OCT-2001 BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone DI30070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                 Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki
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/note="Yector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at be 3' end"
125 c 156 g 141 t 1 others
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/dev_stage="egg"
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Percent Identity: 94.872
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alignment_block:
US-08-973-363-7 x BB461065
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531 CCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAAAAAGAG
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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Ratio: 4.561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno-H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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//dev_stage="12 days embryo"
/lab_host="psinal"
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/db_xref="taxon:10090"
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SOURCE
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozanae, T., Imotani, K., Ishii
, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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Jyg-MC(B) CDNA Mus musculus CDNA clone G930033J21 3', mRNA sequence.
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Fax: 81-45-503-9216
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                                                                                                                                                                                              /clone="6930033J21"
/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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genes. Genome Res. . 10 (10), 1617-1630 (2000)
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Contact: Yoshihide Hayashizaki
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full-length enriched, mammary gland RCB-0527
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                                                                                                                                                                                                                                Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka,T., Matsuura
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REFERENCE
AUTHORS
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VERSION
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LOCUS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 GAGGCTCAGAGACTTTGTGGTGCG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC 349
                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GluAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 rArgAlaAspTyrLeuIleLysLeu.LeuAsnLysAspLeuAlaArgLys 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone inset of clone in the C
                                                                                                                                                                                                                No sl sequence available.
This clone (DKFZ9313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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                                                                                                                                                                          Berlin-Charlottenburg, GERMAI
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                 German Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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4.195
97.619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .438
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Percent Identity: 83.333
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COMMENT
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US-08-973-363-7 x AL601246
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LOCUS AI890775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nth.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I. M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1924 Std Error: 0.00

Seq primer- Adnut From Cibro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 418.
Location/Qualifiers
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4.359
95.122
                                                                                                                                                                                                                                                                                                                                                                                                                                      -40UP from Gibco
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/dev_stage="adult"
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cDNA-collection"
81 c 86 g 100 t
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Percent Identity: 85.366
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wm95fil.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDL_HUMAN O14646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1;, mRNA sequence.

NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Eukaryota, Metazoa: Chordata, Craniata, Vertebrata; Euteleostomi; Mammalla: Eutheria: Primates: Catarrhini; Hominidae; Homo. 1 (bases 1 to 547)

TITLE

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/lab_host="DH108"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT

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REFERENCE
AUTHORS
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ORGANISM
BASE COUNT
ORIGIN
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC
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                                                                                                                                                                                                                                                                                                                                    Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Y., Sugano, S., Isogai, T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                    Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU125712 NT2RM4 Homo sapiens cDNA clone NT2RM4002061 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
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              /cell_type="teratocarcinoma"
/cell_line="NY2"
/note="Vector: pME18SFL3; mRNA
precursor cells"
a 149 c 196 g 207 t
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4.359
95.122
                                                                                                                /clone="NT2RM4002061"
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                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                Location/Qualifiers
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                                                        NT2 neuronal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE895133
BE895133.1 GI:10358221
EST.
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                                Quality:
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national Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                          /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo (
Average insert size 2 kb. Library constructed by Life
Technologies."
198 t
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/clone="IMAGE:3921087"
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alignment_block:

US-08-973-363-7 x BE895133

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 856)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 856)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Charatorization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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GSS; genome survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db.xref="taxon:99883"
/clone="137608"
/clone=115="0"
/notce="Genoscope sequence ID : COBG103BF04LP1-end : T7"
a 308 c 252 g 206 t 6 others
                                                                   154.00
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                                                                Percent Identity: 79.487
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                 Ratio:
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                                                                                                                                                                                                                                                                                             /clone=lib="NACE:4133129"
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/note="Organ: bone marrow; Vector: phR-LIB (Clontech);
/note="Organ: bone marrow; Vector: Site_2: Sit1 (ggccattatggcc);
/note="Organ: bone cell line RNA.
/note="Organ: bone 
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143.00
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     Percent Identity: 83.333
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LOCUS AW996787
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             Similarity:
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
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           133.50
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Seq.primer: puc 18 forward
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Matsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Location/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                           /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed low stringency conditions."
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Direct Submission

Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL352664.1 GI:8246657
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis
Eukaryota; Mecaoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1122)
1 (bases 1 to 1122)
1 Roest-Crollius, H., Jalllon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1122)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS05T9J 1122 bp DNA linear GSS 26-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 042M09 of library C from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1122)
                                                                                                                           303
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/clone="042M09"
/clone_lib="C"
/note="Genoscope sequence ID : C0BC042AG05C1-end : T7"
a 260 c 301 g 246 t 12 others
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Gaps: 0
Percent Identity: 82.857
     Length:
     29
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Ratio: 4.276 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 79.310
alignment_block: US-08-973-363-7 x CNS05T9J ...
Align seg 1/1 to: CNS05T9J from: 1 to: 1122
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9b_pat:AR029026

9b_pat:AX333515

9b_pr:AF006514

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9b_ov:AF060702

9b_ov:AF060702
                gb_ba:AF282249
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gb_htg:AC094708
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-O-/cgp2_1/USPTO_spool_US08973363/runat_01082002_080050_18581/app_query.fasta_1.638
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9b_in:AC007765
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gb_htg:AC091946
gb_pr:AC026778
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gb_htg:AC092382
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gb_pr:AC012624
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gb_pat:A58686
gb_pat:A58683
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Database length: 1873333701
Search time (sec): 4907.710000
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Query: US-08-973-363-8
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Database: GenEmb
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2. 0e-20
2. 0e-20
3. 8e-19
1. 6e-15
1. 6e-17
1. 6e-17
1. 6e-17
1. 6e-14
4. 7-0e-14
7. 0e-14
7. 0e-14
1. 0e-13
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AROSONIA RATURE PROPERTY AND ARTHUR AND ARTHUR AROSONIA Sequence 3 from pater 1414 | ANNOSONIA Sequence 4024 from pater 1464 | ANNOSONIA Sequence 4024 from pater 1464 | ANNOSONIA Sequence 4024 from pater 1764 | AFROGESIA Homo sapiens Chromosonia Sequence 17951 | ACONTAL Homo sapiens Chromosonia Sequence 18029 | ACONTAL HOMO SAPIENS CHROMOSONIA SEQUENCE 1800 | ACONTAL HOMOSONIA 
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1316 | A58996 Sequence | 15 from Patent |
6608 | A58996 Sequence | 10 from Patent |
6608 | A5891 Sequence | 10 from Patent |
6872 | AF004397 Gallus gallus chromo-
153 | A5861 Sequence 3 from Patent |
153 | A58685 Sequence 4 from Patent |
153 | A58685 Sequence 5 from Patent |
153 | A58686 Sequence 5 from Patent |
153 | A58686 Sequence 5 from Patent |
153 | A58686 Sequence 2 from Patent |
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165 | AC01262 Homo sapiens Chromo |
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175 | AC02178 Homo |
175 
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LOCUS A58691
DEFINITION Sequence 10 fr
ACCESSION A58691
VERSION A58691.1 GI:3
KEYWORDS
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gb_htg:AC101378.
gb_ov:OTU89945
gb_pat:AX286188
gb_htg:LMFLCHR36_25
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AUTHORS
TITLE
                COMMENT
FEATURES
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US-08-973-363-8 x A58696
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Ratio: 5.000
Percent Similarity: 100.000
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108.12
137.42
139.02
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Align seg 1/1 to: A58696 from: 1 to: 1316
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A58691
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Location/Qualifiers
1, .1316
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Sequence 15 from Patent WO9639505.
A58696
                                                                                            1 (bases 1 to 6608)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                    Patent: WO 9639505-A 10 12-DEC-1996;
ISIS INNOVATION (GB)
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publication AU 5906996 961224
Location/Qualifiers
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/db_xref="taxon:32644"
a 205 c 308 g 30
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Gaps: 0
Percent Identity: 100.000
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REFERENCE
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VERSION
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LOCUS AF004397
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ORIGIN
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Ratio: 5.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani Phasianinae; Gallus.

1 (bases 1 to 6872)

1 (bases 1 to 6872)

A CHD1 gene is Z chromosome linked in the chicken Ga Gene 197 (1-2), 225-229 (1997)

97473516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
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AF004397.1
                                                                                                                                                                                                                                                                                                                                       Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
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/protein_id="AAC60282.1"
/db_xref="G1:2501846"
/db_xref="G1:2501846"
/translation="MMHSDEESVRNSSGESSRSDDDSGSAGSGSGSSSGSSSDGSSSGSSSDGSSSDSSGSSSDSSGSSSDSSGSSSDSSGSSSDSSSGSSSDSSSGSSSDSSSGSSSDSSSGSSDSSSSDSSSGSSDSSSSDSSSGSSDSSSSDSSSEDSADDSSSETKKKHKDEDWOMSGSGSSSSGTGSLKKCOOOOOKAASSDGSSEEDSSSSEDSADDSSSETKKKHKDEDWOMSGSGSSSGSGTGSLKKCOOOOOKAASSDGSSEEDSSSSEDSADDSSSETKKKHKDEDWOMSGSGSSSGSTGS
                                                                                              /product="chromo-helicase-DNA-binding on the Z chromosome protein" \label{eq:decomposition}
                                                                                                                                                                                                          /gene=
228. .
                                                                                                                                                                                                                                                           /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:32644"
1207 c 1459 g 1
                                                                                                                                                 /function="role in chromatin archite
/note="CHD protein with hydrophilic
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1. .6872
                                                                                                                                /codon_start=1
                                                                                                                                                                                         /gene="CHD-Z"
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on the Z chromosome
(CHD-Z) mRNA, complete
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SOURCE
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US-08-973-363-8
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                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_pat:A58684
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                                                1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                                                                                                                                                                        Sequence 3 from Patent W09639505
A58684
                                                                                                                                                               unidentified unidentified
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Patent:
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MIRTHEWMHPQTKRIKENILLTTYEILLKDKS TLGGLWAPGNAVVLGDITSRN
MIRTHEWMHPQTKRIKENILLTTYEILLKDKS TLGGLWAPGNAVVLGDITSRN
RTLIDFKSNHRLLTTGT PLQNSLKELWSLLHFINPEKFSSWEDFEEHGKGREYGYAS
LHKELEPFLLRRVKKDVEKSLLAKVEQLIRMENSALQKGYYKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCNHCYLIKPDDNEFYNKQEALQHLIRSSGKLILLDKLLILRL
ERGNRVLIFSQMVRMLDILAFYLKYRQPFQRLDGSIKGELKKQALDHFNAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWHPQNDLQAQARAHRIGGKCVNIYRLVTWGS
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HLHKKIKTEKENEEKFEPDIGITKEABEEKFETKEKENKRELKEKEKEKEKE
HLHKKIKTEKENEEKFEPDIGITKEABEEKRETKEKENKKEKEEDKELKEKE
NKEKRENKVERSTQKEREKVEREKVERKSKKILPLDTPVHITATSEPVHISE
WO 9639505-A 3 12-DEC-1996;
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AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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HRSPFEHSSDHKSTPEHTWSSRKT"
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KEYTNPEQIKQMRKNLMIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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                                                                                                                                                                                                                                                 GI:3714247
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1223 c ]
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BASE COUNT ORIGIN

VERSION KEYWORDS

DEFINITION

4180

4130

ACCESSION

REFERENCE

JOURNAL TITLE

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COMMENT
FEATURES
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AUTHORS
                                                                   alignment_block:
US-08-973-363-8 x A58685
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US-08-973-363-8 x A58684
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Ratio: 4.634
Percent Similarity: 80.392
                                                                                                                          Quality: 190.00
Ratio: 4.634
Percent Similarity: 80.392
                                    Align seg 1/1 to: A58685 from: 1 to: 153
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101 AATTACTGAATAAAGACTTGCAAGAAAGAAAGCACAAAGCCTTCCTGGT 150
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1 IleLeuProAspAspProAsp....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified.
unidentified
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Other publication AU 5906996 961224.
Location/Qualifiers
1.153
                                                                                                                                                                                                                                                                                                                                          Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                           Patent: WO 9639505-A 4 12-DEC-1996; ISIS INNOVATION (GB)
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/db_xref="taxon:32644"
a 40 c 31 g 24
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36 c 31 g 30
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LOCUS MUSCHD1x
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
A mammallian DNA-binding protein that contains a chromodomain and an SNE2/SWI2-like helicase domain
Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5349 bp mRNA linear F
Mouse DNA-binding protein (CHD-1) mRNA, complete cds.
L10410 X66028
L10410.1 GI:455014
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TIKQQWWGMKLINIKKKODETKKWIKINASPEDVETYNQQEITIDDLIKQYQTVERI
TAHSNQKSAGLEDYYCKWQGLEYSBCSWEDGALISK KFQTCIDEYSGRNQSKTYPFK
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SVEEDILERAKKKWILDHIVIGRMOTTGRTVLHTGSAPSSSSTFFNKEELSAILKFGAE
ELFKEPEGEEQEPOEMOIDEILKRAETHENEEGFLSCYGDELLGGFKVANFSNMOEDDI
ELFERNKKKWEETIPEGQRRAEBEEEROKELEEITYHLFRANKOISTRAGSKORSK
ELFERNSKKWEETIPEGGRAEBEEROKELEETYHLFRANKOISTRAGSKERELERI
ELFERNSKKWEETIPEGGRAEBEEROKELEETYHLFRANKOISTRAGSKERELERI
SKERSGSSDSISERKREKKRGRERTIFRENIKGFSDAEIREFKSYKKEGEPLERL
SKERSGSSDSISERKREKKRGRERTIFRENIKGFSDAEIREFKSYKKEGEPLERL
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DCRVGRKGATGATTTIYAVEADGDPNAGFERNKEPGDIQY LIKWKGWSHIHNTWETEE
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SDSESEEERDKSSCDGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
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171. .5306
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VQVNAKLVIAHEDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG IYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREA QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLMIFVSKFTEFDARKLH

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REFERENCE
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ORIGIN
                                                      alignment_block:
US-08-973-363-8 x A58686
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ORGANISM
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US-08-973-363-8 x MUSCHD1X
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Ratio: 4.561
Percent Similarity: 100.000
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Ratio:
Percent Similarity:
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IleLeuProAspAspProAsp.
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
BIRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5 from Patent WO9639505.
                                                                                                                                                                                                                                                                                 Patent: WO 9639505-A 5 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                                                                                                                                                   unidentified
                                                                                                                                                                                                                                                                                                                                                                                                  unidentified.
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QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD
HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
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4.439
80.392
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a 1067 c 1319 g 1224 t
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34 c 31 g
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                                 seq_documentation_block:
LOCUS AF006513
                                                                  seq_name:
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US-08-973-363-8 x A58683
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                       DEFINITION
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Homo sapiens CHD1 mRNA, AF006513
AF006513.1 GI:2645428
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Sequence 2 from Patent W09639505
A58683
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c publication AU 5906996 961224
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AUTHORS
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                              alignment_block:
US-08-973-363-8 x AF006513
                                                                                                                          alignment_scores
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Align seg 1/1 to: AF006513 from: 1 to: 5947
                                                                             Percent Similarity:
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TITLE
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1 (bases 1 to 5947)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
                                                                                            Quality:
Ratio:
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                                                                             4.359
95.122
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1 1004 c 1243 g 1570 t
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YHDHHKDRHOGDSYKKSDSRKRPYSSFSNGKDHRDADHYKODSRXYSDREKHRKLDDH
RSRDHRSNLEGSIKDRSHSDHRSHSDHRLHSDHRSSSEYTHKSSRDYRYHSDMQMDH
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/db_xref="taxon:9606"
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/db_xref="GI:2645429"
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                                                                           Percent Identity: 85.366
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26932 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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                    1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US;
3 (Dases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Location/Qualifiers
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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DOE Joint Genome Institute.
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/clone="RP11-58M12"
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/db_xref="taxon:9606"
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                                                                                                        118297 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAAAAAG 118346
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                                     AAGCT.....CTTTCTGGTGCG 118363
gb_htg:AC021449
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DOE Joint Genome Institute.
Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459;
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624
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4 (bases 1 to 1134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 134743 bases at least Q40 Consensus quality: 139227 bases at least Q30 Consensus quality: 140814 bases at least Q30 Consensus quality: 140814 bases at least Q20 Insert size: 14400; sgarose-fp Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1;
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                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will
                                                                                                                                                                                                                        be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 143079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: L5154
Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome
3821 38920: contig of 38820 bp in length
3821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nusbaum, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear HTG 10-SEP-2000 WORKING DRAFT SEQUENCE, 10 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooke, P.,
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alignment_block:
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seq_name: gb_htg:AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                       Quality: 170.00
Ratio: 4.359
Percent Similarity: 95.122
                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AC021449 from: 1 to: 143079
                                                                                                                                                                                                                                                                                                                                   US-08-973-363-8 x AC021449
                                       116247 AAGCT.....CTTTCTGGTGCG 116263
                                                                                                                     116147 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 116196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                            34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                                                               40512 43279: contig of 2768 bp in length
43280 43379: gap of 100 bp
43380 46905: contig of 3526 bp in length
46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
51831 51930: gap of 100 bp
51931 62619: contig of 10689 bp in length
62620 62719: gap of 100 bp
62720 75408: contig of 12689 bp in length
75409 75508: gap of 100 bp
75509 92516: contig of 17008 bp in length
92517 92616: gap of 100 bp
92517 92616: gap of 100 bp
92517 106409: contig of 13793 bp in length
106410 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length
Location/Qualifiers
1 143079:
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62720...75408
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1 26246 c 26678 g 45278 t
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92617 .106409
/note="assembly_fragment"
106510 .143079
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51931. .62619
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47006 .51830
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43380. .46905
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40512..43279
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75509. .92516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-58M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:left"
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1. .38820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                    Length: 41
Gaps: 1
Percent Identity: 85.366
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JOURNAL
REFERENCE
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AUTHORS
TITLE
alignment_scores:
Quality: 170.00
                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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VERSION
KEYWORDS
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LOCUS AC008531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 14374 bases at least Q20
Consensus quality: 14374 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
**NOTE: This is a 'working draft' sequence. It currently
** consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pleces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

** This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 56175 56274; gap of unknown length
* 100975 113127; contig of 44600 bp in length
* 100975 113127; contig of 49630 bp in length
* 11328 118190; cap of unknown length
* 11328 118190; gap of unknown length
* 118291 119694; contig of 1404 bp in length
* 118291 119694; contig of 3503 bp in length
* 113298 123397; gap of unknown length
* 113298 123397; gap of unknown length
* 113298 123397; contig of 3503 bp in length
* 113298 123397; contig of 3503 bp in length
* 123298 123397; contig of 3503 bp in length
* 123298 123397; contig of 3503 bp in length
* 123598 123597; contig of 3503 bp in length
* 123598 123597; contig of 3503 bp in length
* 123598 12559; contig of 2266 bp in length
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1 (bases 1 to 145659)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                         /organism="Homo sapians"
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//chromosome="5"
//chromosome="5"
//clone="07C-480B11"
//clone="07C-480B11"
//clone="07C-480B11"
//clone="07C-480B1 human BAC library C"
//clone_lib="0alTech human BAC library C"
//clone_lib="0alTech human BAC library C"
//clone_lib="0alTech human BAC library C"
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                                                                                                                                                                                                       Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; agarose-fp estimation
**NOTE: This is a 'working draft' sequence. It currently
**consists of 33 contigs. The true order of the pieces
**is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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Center Project Name: 544799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
  170.00
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                                                                                                                                                      /clone="RP11-36012"
/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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                                                                                                                                                                                                                                                                                                                                                        74232: gap of unknown length
79795: contig of 5563 bp in length
79895: gap of unknown length
87511: contig of 7616 bp in length
87511: gap of unknown length
92791: gap of unknown length
92891: gap of unknown length
102794: contig of 9903 bp in length
102794: contig of 9903 bp in length
102894: gap of unknown length
110866: contig of 7972 bp in length
110966: gap of unknown length
110571: contig of 6605 bp in length
117571: gap of unknown length
117572: contig of 6067 bp in length
117671: gap of unknown length
123738: contig of 6067 bp in length
13388: gap of unknown length
130838: gap of unknown length
130838: contig of 10861 bp in length
141644: gap of unknown length
141644: gap of unknown length
169109: contig of 72465 bp in length
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AUTHORS
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alignment_block:
US-08-973-363-8 x AC026778/rev
                                                                                                                                                                      BASE COUNT
ORIGIN
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                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
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ORGANISM
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LOCUS AC026778
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ACCESSION
                                                     Quality: 170.00
Ratio: 4.359
Percent Similarity: 95.122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                     Direct towns.

Submitted (01-JUN-2001) DDE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jun 1, 2001 this sequence version replaced g1:13677045.

Draft Sequence Produced by DOE Joint Genome Institute

WWW.jg1.doe.gov

Finishing Completed at Stanford Human Genome Center

WWW-shgc.stanford.edu

Ouality: Phrap Quality >-40 99.9% of Sequence;

Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195433 bp DNA linear PRI 01-JU
HOMO Sapiens chromosome 5 clone CTC-428I11, complete sequence
AC026778
AC026778.4 GI:14277282
                                                                                                                                                                                                                                                                                                                         SHGC-103595 G57841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 195433)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 195433)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens
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                                                                                                                                                                                   /organism-"Homo sapiens"
/db.xref."taxon:9806"
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/chone="CTC-428II1"
a 37302 c 37040 g 58329 t
                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .195433
                                                       Length: 41
Gaps: 1
Percent Identity: 85.366
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Owery length: 41
Database: N=Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
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Query: US-08-973-363-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
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-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXY-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCt
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000
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-USCR-US0873363-QCG11_1 186 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-973-363-8 to: N_Geneseq_032802:*
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US-08-973-363-8 x AAT42754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 205.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAT42754 from: 1 to: 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                              17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
                                                                                                                                                                                                                                           1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                     ATTTTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGAC
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Length: Gaps: Percent Identity:

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seq_documentation_block:
ID AAT42754 standard; cDNA; 1316 BP.
XX
AC AAT42754;
XX
Chicken CHD-W gene (partial sequency
XX
Bird; sex determination; chromodoma
KW CHD-W; chromodomain-Helicase-DNA bin
XX
Gallus sp.
XX
WO9639505-All.
XX
Gallus sp.
XX
(ISIS-) ISIS INNOVATION LTD.
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(ISIS-) ISIS INNOVATION LTD.
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(ISIS-) ISIS INNOVATION LTD.
XX
XX
Cristiths R, Tiwari B;
XX
Cristiths R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42754
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAF90032 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAF86431 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABI26659 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:AAS74806 +
                                                                                                                                 The chicken CHD-W gene (ANT42754) acting alone or in conjunction with the closely related CHD-LA gene (ANT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-LA gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-LA give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
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94.
73.
131.
128
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1238

34

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seq_documentation_block:
ID AAT42751 standard;
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                                                                               alignment_block: US-08-973-363-8 \times AAT42751
                                                                                                                                                                 alignment_scores:
                                                     Align seg 1/1 to: AAT42751
                                                                                                                         Ratio:
Percent Similarity:
4080
                                                                                                                                                                                                                                             The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken CHD-1A gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT42751;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1996;
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                                                                                                                                                                                                         Sequence 6608 BP;
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                                                                                                                                                                                                                                   acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS
              ATTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex determination; chromodomain-Helicase-DNA binding
; chromodomain-Helicase-DNA binding on the W chromosor
                                                                                                                                                                                                                                                                                                                                                                                                                                  chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tiwari
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                                                                                                                                                                                                         2289 A;
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Gaps:
Identity:
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                                                                                                                                                                                                           1653 T; 0 other;
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100.000
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4129
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17

rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG

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seq_documentation_block:
ID AAT42757 standard;
                                              alignment_block: us-08-973-363-8
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                                                                                                                 alignment_scores:
                                                                               Quality:
Ratio:
Percent Similarity:
                       Align seg 1/1
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                                                                                                                                                                                                                                                                                 Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09639505-A1
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                                                                                                                                                      Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                                                              Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS INNOVATION LTD
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1 IleLeuProAspAspProAsp..
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                                                                                                                                                                                                                                                                                                          chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex determination; chr
A; CHD-W; W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp.
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                        to:
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                                               AAT42757
                        AAT42757
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                                                                               190.00
4.634
80.392
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                                                                                                                                                      58 A; 40 C;
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                        from:
                                                                                Percent
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seq_documentation_block:

ID AAT42758 standard; DNA; 153 BF
XX

AC AAT42758;

XX

Chick CHD-W gene fragment.

XX

Chick CHD-W gene fragment.

XX

Bird; sex determination; chror

XX

Bird; sex determination; chror

XX

Gallus sp.

Location/Qual;

FT misc_difference 52.81

YT

XX

Gallus sp.

XX

YA

WO9639505-A1.

XX

AVA

12-DEC-1996; 96WO-GB01341.

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12-DEC-1996; 95GB-0011439.

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Cisis-) Isis innovation LTD.

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XX

Avian chromodomain-helicase-D

XX

Bases 3855-3977 (AAT42756) of

CC birken S: Fig 3; 76pp; English

XX

Claim 8: Fig 3; 76pp; English

XX

Avian chromodomain-helicase-D

XX

Avian chromodomain-helicas
   alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                        Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to Identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
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                                                                                                                                               BP; 56 A; 36 C;
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52..81
/*tag= a
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"bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
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                                                                                                                                            G; 30 T; 0 other;
Length:
Gaps:
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amino
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42759
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Bases 3855-3977 (AAR142756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAR14757), chicken CHD-W (W refers to the W chromosome) gene (AAR142758) and and the great tit CHD-W gene (AAR142759). Translated amino acid sequences of this region are provided in AAW04164-49. The CHD-1A (see also AAR142751) and CHD-W (see also AAR142754) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding CHD-lA; CHD-W; W chromosome; ss.
                                                                                                           Claim 8; Fig 3; 76pp; English.
                                                                                                                                     Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
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                                                                                                                                                                              1997-043127/04.
DB; AAW08149.
                                                                                                                                                                                                                                                  INNOVATION LTD
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                                                                                                                                                                                                                                                                                                    96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.392
                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 153 BP
                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment.
                                                                                                                                                                                                                                                                                                                                                                       a
*bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identity: 80.392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç
o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                 22-51
amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                     in
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foetus etc. and

to manipulate the

sex of progeny.

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alignment_block:
US-08-973-363-8 x AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SXC
                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAT42756 standard;
                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
Claim
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 153
                                                                Griffiths R,
                                                                                                                05-JUN-1996;
                                                                                                                                12-DEC-1996
                                                                                                                                               W09639505-A1
                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                      Mus sp
                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1; CHD-W; W Chromosome; ss.
                                                                                                                                                                                                                                                            Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                            12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                   151
                                         P-PSDB;
                                                WPI; 1997-043127/04.
                                                                                (ISIS-) ISIS
                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ш
                                                                                                                                                                                                                                                                                                                                                                                                                GCA 153
                                                                                                                                                                                                                                                                                                                                                                  Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                chromodomain-helicase-DNA binding genes determine sex
- used for sex determn. and to control sex of progeny
8; Fig 3;
                                         AAW08146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B₽;
                                                                                INNOVATION LTD
                                                               Tiwari
                                                                                                95GB-0011439
                                                                                                               96WO-GB01341
                                                                                                                                                                                     Location/Qualifiers 52..81 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182.00
4.439
80.392
76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                            "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \frac{\omega}{\omega}
                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
                                                                                                                                                                                                                                                                                                            ₽P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Gaps:
L Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                      22-51
amino
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                         'n
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*22222222222
*222222222222
seq_documentation_block:
ID AAV59280 standard; cDNA; 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-973-363-8 x AAT42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AACTACTTAGCAGAGATCTTGCAAAAAGAGAGGGCTCAGAGACTTTGTGGT
                                   04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                               CDS
                                                                                                                                                                                                                     Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                            14-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 153 BP;
         (UYRQ ) UNIV ROCKEFELLER
                                                                         13-FEB-1998;
                                                                                                   20-AUG-1998
                                                                                                                            WO9836066-A1
                                                                                                                                                                                                                                                         telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                                                                                                                                                                                                                        ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                               Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                      AAV59280;
                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42756
                                   98US-0018628
97US-0800264
                                                                          98WO-US02765
                                                                                                                                                     /*tag= a
/product= "A-TRF"
                                                                                                                                                                               Location/Qualifiers
1..1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172.00
4.195
80.392
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                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ი</u>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.588
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seq_documentation_block:
ID AAK88882 standard; cDNA; 42
XX
AC AAK88882;
XX
DT 05-NOV-2001 (first entry)
XX
Human digestive system anti
XX
Human; digestive system anti
XX
Human; digestive system anti
XX
Human; digestive system disorder;
XX
digestive system disorder;
XX
HOMO sapiens.
XX
PN W0200155314-A2:
XX
PD 02-AUG-2001.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2000; 2000US-01790658
PR 04-FEB-2000; 2000US-01805628
PR 04-FEB-2000; 2000US-0186580
PR 04-FEB-2000; 2000US-0186580
PR 04-FEB-2000; 2000US-0186580
PR 04-FEB-2000; 2000US-0186580
PR 16-MAR-2000; 2000US-0186580
PR 16-MAR-2000; 2000US-01805974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-973-363-8 x AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK888882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 129.00
Ratio: 5.160
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The altered vertebrate telomere repeat binding protein (A-TRE) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRE, preventing it from binding to the specified repeat sequence. A-TRE, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atheroscierosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                         Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                        Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW59280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-480769/41.
                                                                                                                         17-JAN-2001; 2001WO-US01324
  2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Lange
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Steensel B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 25
Gaps: 0
Percent Identity: 100.000
      11-JUL-2000

14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

15-AUG-2000

16-SEP-2000

17-SEP-2000

18-SEP-2000

18-SEP-2000

19-SEP-2000

10-SEP-2000

10-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0198076
2000US-0198123
2000US-0205515
2000US-0215815
2000US-0214886
2000US-02116647
2000US-0217496
2000US-0217496
2000US-0217496
2000US-0217496
2000US-0224518
2000US-0224518
2000US-0224518
2000US-0225213
2000US-0225213
2000US-0225216
2000US-0225213
2000US-0225216
2000US-0225217
2000US-0225217
2000US-0225217
2000US-0225217
2000US-0225217
2000US-0225266888
2000US-022575886888
2000US-02257182
2000US-02257182
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17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 - CCT - 2000
20 - NOV - 2000
21 - NOV - 200
                                Claim 1;
                                                                 digestive system, particularly
                                                                                 Polynucleotides encoding diagnosing, treating, pre
                                                                                                                                                                                        Rosen
                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                       (HUMA-) HUMAN
                                                                                                                                     2001-502630/55
DB; AAM93109.
                                SEQ
                                                                                                                                                                                       Barash
                                                                                                                                                                                                                                                       2000US-0239937
2000US-0241956
2000US-0241785
2000US-0241785
2000US-0241808
2000US-0241808
2000US-0244617
2000US-0246475
2000US-0246476
2000US-0246476
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2000US-0246511
2000US-0246511
2000US-0249211
2000US-0249216
2000US-0249218
2000US-0249264
2000US-02511868
2000US-02511868
2000US-02511899
2000US-02514997
2000US-02514997
                                 H
                                                                                                                                                                                                                        GENOME
                                NO 1198;
                                                                                                                                                                                        SC
                                                                                                                                                                                                                        SCI INC
                                                                              ing digestive system antigens, useful for preventing and/or prognozing disorders o
                                                                                                                                                                                       Ruben
                              986pp;
                                                                                                                                                                                        MS
                                                                 cancer and
                                English
                                                                 cancer
                                                                 metastases
                                                                                0f
                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg
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The present invention provides the protein and coding sequences

of.

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SSSSSSSSS
  seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAI57603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-973-363-8 x AAK88882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block:
AAI57603 standard; cDNA; 421 BP
31-JAN-2000

04-FEB-2000

04-FEB-2000

12-MAR-2000

11-MAR-2000

11-MAR-2000

11-MAR-2000

11-MAY-2000

07-JUN-2000

07-JUN-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digest.
                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                 Human; colorectal cancer; colorectal cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                         Human colorectal cancer antigen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                        AAI57603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 GGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 421 BP; 148 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system antigen of the invention.
                                                                                                                                                                                                                                                      17-JAN-2001;
                                                                                                                                                                                                                                                                            02-AUG-2001
                                                                                                                                                                                                                                                                                                   WO200155350-A1
                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 CCGAGCGGATTACTTGTTGAAGCTGCTCAGAAAGGGTCTGGAGAAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 luAla
                                                                                                                                                                                                                                                                                                                           sapiens
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
2000US-0186350
2000US-018974
2000US-0199076
2000US-0198123
2000US-0205515
2000US-020467
2000US-0214886
2000US-0216647
2000US-0216680
2000US-0217496
2000US-0217496
2000US-0218990
2000US-02189963
2000US-0229643
2000US-0229643
2000US-02245189
2000US-02245189
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                       2000US-0180628
2000US-0184664
                                                                                                                                                                                                                               2000US-0179065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK88882
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4.067
85.714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
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Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G;
                                                                                                                                                                                                                                                                                                                                                                         SEQ
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2000US-0225213 2000US-0225214

2000US-0225268 2000US-0225270 2000US-0225447 2000US-0225757 2000US-0225758 2000US-0225759 2000US-0226681 2000US-0226868 2000US-0226868 2000US-0226868 2000US-0226868 2000US-0226868 2000US-0228868 2000US-0228868 2000US-0228868 2000US-0228868

2000US-0229343. 2000US-0229344. 2000US-0229345.

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alignment_scores:
Quality:
Ratio:
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17-NOV-2000
01-DEC-2000
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06-DEC-2000
08-DEC-2000
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17-NOY-2000
17-NOY-2000
17-NOY-2000
                                                                                                                              The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AALS75619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention
                                                                                                                                                                                                                               Isolated polypeptide for disorders related to the and also for testing and
                                                                                   The present sequence is a colorectal cancer antigen coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                             Sequence
                                                                                                                                                                                                           Claim 1; SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
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7-NOV-2000;
7-NOV-2000;
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7-NOV-2000;
7-NOV-2000;
7-NOV-2000;
7-NOV-2000;
7-NOV-2000;
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DB; AAM38625.
                                                              421 BP;
                                                                                                                                                                                                                                                                                                                       Barash
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2000US-0246524

2000US-0246526

2000US-0246532

2000US-0246610

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2000US-0246611

2000US-0249209

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2000US-0249216

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2000US-0251868

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2000US-0251989
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4.067
                                                             148 A; 78
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                                                                                                                                                                                                                               treating, preventing and/ or prognosing colon and rectum including colorectal coefficient e.g. diagnosis .
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                                                             127
                                                            G; 61 T;
 Length:
Gaps:
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                                                              other;
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14-AUG-2000
11-AUG-2000
11-AUG-2000
11-AUG-2000
11-SEP-2000
11-SEP

2000US-0229509 2000US-0230431 2000US-0230438 2000US-0231243 2000US-0231244 2000US-0231414 2000US-0231411 2000US-0231414 2000US-0232080 2000US-0232081 2000US-0232081 2000US-0232398 2000US-0232399 2000US-0232399 2000US-0232399 2000US-0232399 2000US-0232399 2000US-0232399 2000US-0232401 2000US-0232401 2000US-0232401 2000US-0233064 2000US-0233064 2000US-0233064 2000US-0233064 2000US-0233064 2000US-02344274 2000US-02344274 2000US-02344274

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2000US-0241787
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2000US-0241808
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2000US-0241806
2000US-0244876
2000US-0244475
2000US-0246476
2000US-02464778

alignment_block: US-08-973-363-8 x ABL06443

Ratio: Percent Similarity:

Quality:

88.00 2.839 81.579

Gaps: Percent Identity:

55.263

Align seg 1/1

to:

ABL06443

from:

ţo:

6240

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seq_documentation_block:
ID ABL06443 standard:
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US-08-973-363-8 x AAI57603
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                                                                     capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL018176-ABL30511), expressed DNA sequences (ABL018737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
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                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                      Venter
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11-JUL-2000;
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Sequence
                                          The sequence data for this patent did not form specification, but was obtained in electronic :
                                                                                                                                                                                                                                    interactions
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                            ftp.wipo.int/pub/published_pct_sequences
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CCGAGCGGATTACTTGTTGAAGCTGCTCAGAAAGGGTCTGGAGAAGAAGG 20
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 6240
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                                                                                                                                                                                                                                                                                                                                                                                           2000US-191637P.
2000US-0614150.
 BP;
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1682 C;
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alignment_scores:

Sequence 9933 BP;

2711

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2468 C;

2538

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seq_documentation_block:
ID ABL06442 standard; cDNA;
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                                       specification,
                                                                              cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG11), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins
                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling
                                                                                                                                                                                           Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
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                                                    The sequence data for this patent did not form
                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
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11-JUL-2000;
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                        ftp.wipo.int/pub/published_pct_sequences
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alignment_block:
US-08-973-363-8 x ABL06442
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Percent Similarity:
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Sequences AAS59506-AAS59804 represent DNA molecules encoding propionibacterium acmes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acmes. The disorders include SAPHO syndrome (synovitis, acme, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acmes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acme vulgaris. A method for detecting the presence or absence of P. acmes in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                              Propionibacterium acmes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acme vulgaris -
                                                                                                                                                                Claim 1; SEQ ID No 85; 1069pp; English.
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81.579
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, Jen S, Carter D;
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Gaps: 2
Percent Identity: 55.263
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seq_documentation_block:
ID AASS6071 standard; cDNA; 1908 BP.
XX
AC AAS96071;

XX

26-FEB-2002 (first entry)
XX

DT 26-FEB-2002 (first entry)
XX

Leishmania antigen 4G2-83 extended:
XX

Leishmaniasis; Leishmania antigen; Lbhsp83
XW MAPS-lA; LmgSP3; LugSP3; LugSP
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7395 CTGGGAGACGTGTAGCGGGA 7414
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmaniasis; Leishmania antigen; immunostimulant; protozoacide; Ldp23; interleukin-15; PCR primer; Lbhsp83; M15; Lt-1; LbeIF4A; Lmsp1a; Lmsp9a; MAPS-1A; LmgSP1; LmgSP3; LmgSP5; LmgSP8; LmgSP9; LmgSP1; LsgSP1; S; LcgSP1; LcgSP3; LcgSP4; LcgSP8; LcgSP10; IG6-34; IE6-44; 4A5-63; IB11-39 2A10-37; 4G2-83; 4H6-41; 8G3-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leishmania antigen 4G2-83 extended DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12928 BP; 2564 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 luAlaGlnArgLeuAlaGly
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                                                                                                                   Skeiky YAW,
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Example 2;

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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polypeptides comprising an immunogenic part of Leishmania antigen. The Leishmania polypeptides and their associated DN sequences, epitopes and fusion proteins are used in the production of compositions used for inducing a protective immune response against leishmaniasis, for prevention and treatment of the disease. The compositions can also be used generally to treat diseases that respond interleukin-15 stimulation. In addition, the products may contain an immunostimulant. The sequences represent cDNA molecules encoding Leishmania antigens and PCR primers used to amplify DNA of the invention
                                                                                                                                                                                                                                                                                           subunit vaccine; nucleic acid immunisation; gene therapy; genetic disease; hemophilia; cystic fibrosis; cancer; viral infection; acquired immune deficiency syndrome; PAV antigen; porcine pathogen; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Leishmania antigens, useful diagnosis of leishmaniasis, also related
New nucleic acids from the genome of porcine adenovirus-3, gene therapy vectors, particularly for immunization
                                                                                                                                                                                                     21-OCT-1999
                                                                                                                                                                                                                                   W09953047-A2
                                                                                                                                                                                                                                                                Porcine adenovirus
                                                                                                                                                                                                                                                                                                                                          PAV-3;
                                                                                                                                                                                                                                                                                                                                                                    Complete nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA230163 standard;
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                                                 WPI; 1999-620422/53
                                                                                                                                           15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Page 190;
                                                                                                                                                                                                                                                                                                                                       defective recombinant PAV vector; live recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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                                                                             Tikoo SK,
                                                                                                             SASKATCHEWAN.
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89.474
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                                                                               Babiuk LA;
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seq_documentation_block:
ID AAX39679 standard; DN
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AC AAX39679;
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XX
Cancer associated ant
XX
Cancer associated ant
XW breast cancer; colon
XW prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN W09904265-A2.
XX
PD 28-JAN-1999;
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PD 28-JAN-1999;
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PF 15-JUL-1998; 98WO-U
XX
PR 17-JUL-1997; 97US-0
PR 17-JUL-1997; 97US-0
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US-08-973-363-8 x AAZ30163/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a defective recombinant PAV vector comprising inverted terminal repeats (ITR), packaging sequences and at least one heterologous nucleotide sequence (II), but lacking El functions. The defective vectors replicate inefficiently in cells (other than helper cells) so are unlikely to be immunogenic. Deletion of the El (and optionally other regions) increases the size of heterologous insert that can be packaged. The PAV-3
                                                                                                                                                                                                                                                                           Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                       Renal cancer associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX39679 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides can also be used for diagnosis (to detect PAV-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCAGGACGGCTTCCCACACGCCAAGTACTGGGACAGCGATCAGGAGTA
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                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reverse of: AAZ30163
      98US-0102322.
97US-0896164.
97US-0061599.
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                                                                                                                                               The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnostis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                       1761 GTTTGAGAACCTCTGCAAAATCATG...AAAGACATATTGGAGAAAAAAG 1807
1808 TGAAAAGG 1815
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2911 BP; 957 A; 519 C; 686 G; 749 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 67; Page 496-497; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lung cancer.
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                                  35 laGlnArg 37
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97GB-0021697.
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J, Stockert E;
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jb_estl:ANI125712
jb_estl:RS95133
gb_gss:CNS04DVG
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gb_estl:AN9967967
gb_estl:AN997058
gb_gss:CNS05759
gb_estl:AI49703
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gb_estl:AI49703
gb_estl:AI685364
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Database length: -1841457050
Search time (sec): 4390.400000
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Query: US-08-973-363-8
Query length: 41
Database: EST:*
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-C-/cgn2_1/USSP0_spool/US0897363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST -CPMT-fasta_ SUFFIX-P2n.rst -GAPOP-12.000 -GAPEXT=4.000
-MINMATCH-0.100 -LOOPEL-0.000 -LOOPEXT=0.000 -GAPOP-4.500
-GAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500 -FGAPOP-6.000
-GAPEXT=7.000 -YGAPOP-10.000 -XGAPEXT=0.500 -DELOP-6.000
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-DELEXT=5.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELOP-6.000
-NOLEIGH-15 -MODE-LOCAL -OUTFMT-PIS -NORM-ext -HEARSIZE-500
-NINLEN-10.MAXLEN-200000000 -USER-US0897365_@CGN1_1_2938
-NCPU-6 -ICPU-3 -LONGLOG -DEV_TIMEOUT-120 -MARN_TIMEOUT-30
-NO_XLPXY -WAIT -THREADS-1
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                  250 A 
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Len | Documentation  
593 | AL659353 AL659353 XGC-neurula  
619 | BH15356 BH155356 RIKEN full-le  
644 | BH15356 BH155356 RIKEN full-le  
645 | AL644594 AL644594 XGC-egg Silur  
660 | BH15356 BH3651065 RIKEN full-le  
430 | AL601246 DKFZp313J1040_rl 313  
547 | AL890775 wm95fll.xl NCI_CGAP_Ut  
646 | BH34922 BH3392730 RIKEN full-le  
430 | AL601246 DKFZp313J1040_rl 313  
547 | AL890775 wm95fll.xl NCI_CGAP_Ut  
646 | BH329976 G01905170Fl NIH_MGC_T  
646 | AU125712 AU125712 NW72R4 Homo  
647 | AL9997058 QV3 BN0047-230200-102-  
648 | AW997058 QV3 BN0047-230200-102-  
648 | AW997058 QV3 BN0047-150400-152-  
648 | AW997058 QV3 BN0047-150400-152-  
649 | AL352864 Tetracodon nigroviridi  
334 | AA305759 EST176834 COLon carcin  
346 | AL648536 Tetracodon nigroviridis  
347 | AL352564 Y986h11.sl Scares fetal  
348 | AL648536 Tx55b06.xl NCI_CGAP_CC  
436 | AL648536 Tx55b06.xl NCI_CGAP_CC  
436 | AL648536 Tx55b06.xl NCI_CGAP_CC  
437 | AW354689 pM3-pT0037-231299-001-  
646 | BG777172 607271051111  
647 | AL341950 Tetracodon nigroviridis  
647 | AW354689 pM3-pT0037-231299-001-  
648 | BG737172 fotracodon nigroviridi  
649 | AL341950 Tetracodon nigroviridi  
640 | AL134182 Tetracodon nigroviridi  
640 | AL134182 Tetracodon nigroviridi  
641 | AL134182 Tetracodon nigroviridi  
642 | AL134182 Tetracodon nigroviridi  
643 | AL137122 Tetracodon nigroviridi  
644 | AL137130 Tetracodon nigroviridi  
645 | AL131668 Tetracodon nigroviridi  
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647 | AL131668 Tetracodon nigroviridi  
648 | AL132103 Tetracodon nigroviridi  
649 | AL131668 Tetracodon nigroviridi  
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gb_est2:BM185888
gb_est2:BM070535
gb_est2:BM024825
gb_est2:BM185005
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AUTHORS
TITLE
JOURNAL
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US-08-973-363-8 x AL659353/rev
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4.921
97.436
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1.5e-07
1.5e-07
1.6e-07
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Align seg 1/1 to reverse of: AL659353 from: 1 to:
                                                                                                        296 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG
                             17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                  1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 593)

Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Kenopus tropicalis EST project 2001 (10_2001)

Unpublished (2001)

Contact: Huckle E

Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              western clawed frog.
Silurana tropicalis
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TRODICALIS_EEQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Theu045e20"
/clone=lib="xGC-neurula"
/dev_stage="neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/lab_host="Poctor: PCS107; Site_1: EcoR1; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BEORI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                      Length: 39
Gaps: 0
Percent Identity: 94.872
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| BM185888 fv74a09.x1 z
| BM070535 fu99h05.x1 z
| BM024825 fu73e09.x1 z
| BM185005 fv16c08.x2 z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

On Jun 29, 2000 this sequence version replaced gi:8811286.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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BB155356 2 GI:16268254
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara,
                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, Fukunishi, Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           further details.
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                                                                                                                                                                                                                                                                                                                                                                        mouse tissues
                                        /lab_host="DH10B"
/note="c:-
                                                                                                                                                         thymus
                                  /note="Site_
                                                                                       /tissue_type="thymus"
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                                                                                                                                                                                                                 /clone="A130024L16"
                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched, 16 days neonate
                               1: SalI; Site_2:
sequenced
      'n
      Mouse
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   BamHI; cDNA library was use Genome Encyclopedia
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ORGANISM
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VERSION
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ORIGIN
                                                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
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seq_documentation_block:
LOCUS AL644594
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US-08-973-363-8 x BB155356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 CCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          589 AGGCTCAGAGACTTTGTGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est1:AL644594
                                                                                                                                                                                                                                                  Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.

1 (bases 1 to 645)
                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis
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                                                                                                                                       Sanger Xenopus tropicalis EST project 2001 TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                           Hinxton, Cambridgeshire, CB10 1SA, Email: trop@sanger.ac.uk
                                                                                                                                                                                                                  Sanger Centre
                                                                                                                                                                                                                                     Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                     western clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                          AL644594.1 GI:16796719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                     constructed by Aaron M.
                                                                                                                        Sequencing primer: P1C
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                                                                                                   sequence is from a Xenopus Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
/db_xref="taxon:8364"
/clone="rin":"
                                                                Location/Qualifiers
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LOCUS BB461065
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US-08-973-363-8 x AL644594
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Ratio: 4.921
Percent Similarity: 97.436
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RS Arakawa, T., Carrinct, P., Fukuda, S., Furunco, M., Haragaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Shihata, K., Shihagawa, A., Shiraki, T., Sogabe, Y., Szuki, H., D., Shibata, K., Shinagawa, A., Takahash, F., Takeda, Y., Tanaka, T., Toya, T., Tagami, M., Tagawa, A., Takahash, F., Takeda, Y., Tanaka, T., Toya, T., Muzamatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

AL Unpublished (2001)

On Jul 21, 2000 this sequence version replaced gi:9356558.

Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB461065 TIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-tloring protein (CHD-1) mRNA, mRNA sequence.
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Vector: pcS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
125 c 156 g 141 t l others
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/dev_stage="egg"
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Gaps: 0
Percent Identity: 94.872
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alignment_block:
US-08-973-363-8 x BB461065
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Ratio: 4.561
Percent Similarity: 100.000
581 AGGCTCAGAGACTTTGTGGTGCG 603
                                                                                                                    531 CCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAAAAAAGAG 580
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                                                                                                                                                                          17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit of
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="pH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal ganglion"
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/dev_stage="12 days embryo"
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/db_xref="taxon:10090"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930033J21 3', mRNA
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsu, Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                          Quality:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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e mouse tissues
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URL:http://genome.gsc.riken.go.jp/
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/tissue_type="mammary gland"
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Jyg-MC(B) cDNA N
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                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci, P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
Carninci, P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tawaka,M., Ohara,E.,
wathiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tamaka,T., Matsuu
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9216
                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone inset of Clone from 5. Wateman, Molecular Genome Analysis, German Cancer Research Center (DRF2), Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (Mational Research Center for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.

1 (bases 1 to 430)
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DK725313J1040_r1 313 (synonym: h1cc2) Homo sapiens cDNA clone
DK725313J1040 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                             No sl sequence available.
This clone (DKRZp3l3J1040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
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RCB-0527 Jyg-MC(B) cDNA"
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g6 c 108 g 96 t
/clone="DKFZp313J1040"
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                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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TITLE
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US-08-973-363-8 x AL601246
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LOCUS AI890775
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Ratio:
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95.122
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//dey_stage=#dollt"
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AUTHORS
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US-08-973-363-8 x AI890775/rev
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LOCUS AU125712
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                                                                                                                                                                                                                                                                                                               Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 2
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai,T.
HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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                                                                                                                                                                                                                                       Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers
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       /cell_type="teratocarcinoma"
/cell_line="NT2"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced precursor cells"
a 149 c 196 g 207 t 2 others
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/db_xref="taxon:9606"
/clone="NT2RM4002061"
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alignment_block:
US-08-973-363-8 x AU125712
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  Percent Similarity:
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Ratio:
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; 1
1 (bases 1 to 1028)
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Mammalia; Eutheria; Primates;
                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 488.
Location/Qualifiers
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo of Site_2: SalI; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."
Technologies."
198 t
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4.359
95.122
170.00
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95.122
                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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Gaps:
Percent Identity:
  Percent Identity:
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                      Gaps:
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alignment_block:

US-08-973-363-8 x BE895133

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REFERENCE
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alignment_block:
US-08-973-363-8 x CNS04DVG/rev
                                                                                                      alignment_scores:
Quality:
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                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Peleostei; Euteleostei; Neoteleostei;
Tetraodontidae; Tetraodon.
1 (bases 1 to 856)
1 (bases 1 to 857)
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J. ... 1811ault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J. Brottler, P., Quetier, F., Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS04DVG 856 bp DNA linear GSS 21-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
103K08 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                  /organism-"retraodom nigroviridis"
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4.400
89.744
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Gaps: 0
Percent Identity: 79.487
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REFERENCE
AUTHORS
TITLE
alignment_block:
US-08-973-363-8 x BF239967
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LOCUS BF239967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnThrAr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONETECH Laboratories, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov k column: 18 Plate: LLCM1033 row: k column: 18 High quality sequence stop: 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BukaryOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
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BF239967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                        345
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                                                                        143.00
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                                                        Percent Identity: 83.333
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 337)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Matsukuma, A., Bala, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA,
                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
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Location/Qualifiers
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                                                                                                                                                                                                                      /note-"Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                     tissue mRNA and cDNA amplification were performed low stringency conditions."
59 c 72 g 123 t
133.50
3.926
94.444
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Identity:
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                         /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of
                                                                                                                                     tissue mRNA and cDNA amplification were performed under
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REFERENCE
alignment_scores:
Quality: 124.00
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US-08-973-363-8 x AW997058/rev
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Ratio: 3.629
Percent Similarity: 100.000
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AL352864.1 GI:8246657

AL352864.1 GI:8246657

SGS; genome survey sequence.

Tetraodon nigroviridis
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

DE 1 (bases 1 to 1122)

Tetraodontidae, Tetraodon.

DE 1 (bases 1 to 1122)

Bouneau.L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Reissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSU5T9J 1122 bp DNA linear GSS 26-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 042M09 of library C from Tetraodon nigroviridis, genomic survey sequence
                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1122)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using Terrapdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1122)
                                                                                                                     303 a
                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="042M09"
/clone_lib="C"
/clone_lib="C"
/note="Genoscope sequence ID : C0BC042AG05C1-end : T7"
a 260 c 301 g 246 t 12 others
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Gaps: 0
Percent Identity: 82.857
       Length:
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Percent Similarity: 100.000 Percent Identity: 79.310
alignment_block:
US-08-973-363-8 x CNS05T9J from: 1 to: 1122
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9b_pat: ANO29026

9b_pat: AN333515

9b_pat: AN333515

9b_pr: AP006514

9b_htg: AC087641

9b_htg: AC013394

9b_pr: AC013394

9b_ov: AF060702

9b_in: CEND6001

9b_in: CEND6001

9b_in: AC01985

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9b_in: AC01765

9b_in: AC092187
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gb_pat:A58691
gb_ov:AF004397
gb_pat:A58686
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gb_ro:MUSCHD1X
gb_pat:A58683
gb_pr:AF006513
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Query: US-08-973-363-9
Query length: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: Aug 3, 2002 4:27 AM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database sequences: 1797656
Database length: 1873333701
Search time (sec): 4907.710000
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7.2e-09

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.5e-17
.3e-17
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13465 i AC012624 Homo Sapiens chromd
134075 i AC021424 Homo Sapiens chromd
143079 i AC021424 Homo Sapiens chromd
159446 i AC098531 Homo Sapiens chromd
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270581 i AC022122 Homo Sapiens chromd
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270581 i AC092363 Sequence 3 from Pater
1311 i AR029205 Sequence 4024 from Pat
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17058 i AC087641 Homo Sapiens chromd
181578 i AC013734 Homo Sapiens chromd
181578 i AC0137378 Homo Sapiens chromd
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16 | A58696 Sequence 10 from Patent

172 | AF000397 Gallus gallus chromo-

13 | A58691 Sequence 5 from Patent

13 | A58686 Sequence 5 from Patent W

13 | A58686 Sequence 4 from Patent W

13 | A58688 Sequence 4 from Patent W

14 | L10410 Mouse DNA-binding profes

14 | L10410 Mouse DNA-binding profes

14 | A58683 Sequence 2 from Patent W

14 | L10410 Mouse DNA-binding Profes

14 | A58683 Sequence 2 from Patent W

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gb_in:AF139114
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                                                                                                                                           REFERENCE
AUTHORS
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alignment_block:
US-08-973-363-9 x A58696
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LOCUS A58691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                                                                                                                                                                                                                                                    34 luValGlnArgLeuThrGlyAla 41
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Ratio: 4.805
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Sequence 15 from Patent W09639505.
                                     Patent: WO 9639505-A 10 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                               1 (bases 1 to 6608)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                              unidentified
                                                                                                                                                                                                                                   A58691
A58691.1 GI:3714250
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Sequence 10 from Patent WO9639505.
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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INNOVATION (GB)
r publication AU 5906996 961224
Location/Qualifiers
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1 205 c 308 g
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62.50
62.00
61.50
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Gaps: 0
Percent Identity: 95.122
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122.87
142.28
141.32
108.53
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175.96
14.60
16.51
1.1e+03
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24314 ! AC110387 Rattus norvegicus
2595 ! AF139114 Neospora caninum s
2482 ! AF068773 Danio rerio heat s
73128 ! AC101378 Mus musculus clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 others
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JOURNAL
MEDLINE
REFERENCE
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KEYWORDS
SOURCE
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US-08-973-363-9 x A58691
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ORIGIN
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                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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Ratio: 4.805
Percent Similarity: 100.000
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TITLE
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TITLE
                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGAC
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                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves; Neognathae; Gallii phasianinae; Gallus.

1 (bases 1 to 6872)

Griffiths, R. and Korn, R.M.

A CHD1 gene is Z chromosome linked ir Gene 197 (1-2), 225-229 (1997)

97473516

2 (bases 1 to 6872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF004397 6872 bp mRNA linear VRT 08-OCT-19 Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
                                                                                                                                                                                                                                                                                                      Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                                    Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chicken.
/gene="CHD-2"
/function="role in chromatin architecture"
/functe="CHD protein with hydrophilic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:32644"
1207 c 1459 g 1
                                                                                             protein"
                                                                                                                                                                                                                                      /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                        Cocation/Qualifiers
l. .6872
                                                                                                            /product="chromo-helicase-DNA-binding on the Z
                                                                                                                            codon_start=1
                                                                                                                                                                                            /gene="CHD-z"
228. .5654
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Gaps: 0
Percent Identity: 95.122
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Neognathae; Galliformes;
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                                                                                                              chromosome
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alignment_block:
US-08-973-363-9 x AF004397
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                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_pat:A58686
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Ratio: 4.805
Percent Similarity: 100.000
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                                                1 (bases 1 to 153)
Griffiths,R. and Tiwari,
AVIAN GHD GENES AND THEI
                                                                                                                                                                                                                                                                           Sequence 5 from Patent W09639505
A58686
                                                                                                                                                                 unidentified unidentified
Patent:
                            BIRDS
                                                                                                                                    unclassified
                                                                                                                                                                                                                                                 A58686.1
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WO 9639505-A 5 12-DEC-1996;
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/note="short i:
1 1223 c 15:
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LFKEPEGEEQEPQEMDIDEILKRAETERNEFQFLTVGDELLSQFKVARFSNNDEDDIE
LEPERNSRNWEEIIPESORRRIEEEERQKELEEITMLFRARRCAKOISFNGSBGRRSR
SRRYSGSDSDSITERKRPKKRGRPTIPRENIKGFSDAEIRRIKSYKKFGGFLERLD
AVARDAELVDKSETDLERLGELVHNGCIKALKDNSSGOERAGGRLGKVKGFTFRISGV
QVNAKLVISHEEELAPLHKSIPSDPEERKRYLTPCHTKAAHFDIDWGKEDDSNLLVGI
TEYGYGSWEMIKMDPDLSLTQKILPDDPDKKFQAKQLOTRADYLIKLLNKDLARKEAQ
RLAGAGNSKRRKTRNKKNKNKASKIKEEIKSDSSPQPSEKSDEDEEDNKDEIVSVK
HLHKKIKTEKENEKEPPDIGIK BAADEKRETKEENKKELREKKEEDKKELKEKD
REKRENKVKESTQKEKEVKEEXVNEMSENKEKSKIPLLDTPVHITATSEPVPISE
ESEELHQKTFSVCKERMRPVKAAALKQLDRPEKGLSEREQLEHTRQLIKIOHITECL
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AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
                                                                                                                                                                                                                                                 GI:3714249
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                                                      AND THEIR USE IN METHODS
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Gaps: 0
Percent Identity: 95.122
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BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE

JOURNAL

SOURCE ORGANISM

ACCESSION VERSION DEFINITION

4130

17

4180

KEYWORDS

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REFERENCE
AUTHORS
TITLE
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FEATURES
                                                                                                                    alignment_scores:
Quality: 182.00 Length: 51
Ratio: 4.439 Gaps: 1
Percent Similarity: 80.392 Percent Identity: 76.471
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US-08-973-363-9 x A58686
                                                                      alignment_block:
US-08-973-363-9 x A58684
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KEYWORDS
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ORIGIN
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ORIGIN
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ORGANISM
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Ratio: 4.659 Gaps: 1
Percent Similarity: 80.392 Percent Identity: 80.392
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                                       Align seg 1/1 to: A58684 from: 1 to: 153
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                                                                                                                                                                                                                                                                                                                   source
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101 AATTACTGAATAAAGACTTGCAAGAAAAGAAGTGCAAAGACTTACTGGT 150
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l IleLeuProAspAspProAsp......
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Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified.
unidentified
                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 9639505-A 3 12-DEC-1996; ISIS INNOVATION (GB)
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADUBUTA 153 bp Sequence 3 from Patent W09639505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unclassified.
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60 a 34 c 31 g
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Location/Qualifiers
1. 153
                                                                                                                                                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
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REFERENCE
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US-08-973-363-9 x A58685 , ...
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ORIGIN
DEFINITION Mouse DNA-binding protein (CHD-1) mRNA, complete cds.
                                                                       seq_name: gb_ro:MUSCHD1x
                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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LOCUS A58685
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                                  seq_documentation_block:
LOCUS MUSCHD1x
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                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 80.392 Percent Identity: 76.471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other publication AU 5906996 961224.
Location/Qualifiers
1, 153
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1 (bases 1 to 153)

Griffiths,R. and Tiwari,B.

AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4 from Patent WO9639505.
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US-08-973-363-9 x MUSCHD1X
                                                                                 Percent Similarity:
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Delmas, V., Stokes, D.G. and Perry, R.P.
                                                                                                                                        Quality:
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DNA binding protein.
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Feb 16, 1994 this sequence version replaced gi:293322.
Location/Qualifiers
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ELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNMDEDDI
ELEPERNSKNWEEIIPEEQRRRLEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
                                                                                                                                                                                                                                                                                                                                             QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD
HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK
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DAIARDAELVDKSETDURRLGELVHNGCVALKDSSGSTERAGGRLIGKVKGPTFRISG
VOVNAKLYLAHEDELLPLHKSIPSDEPERKOYTIPCHTKAAHPDIDWGKEDDSNLILD
IYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSSGKLILLDKLLIRL
RERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDF
CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKG
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YKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
SLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSK
                                                                                                                                                                                                                                                                                                                     HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT
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DCKVLKQRPRFVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEMGL
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DDEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEDEEFETIERVM
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/product="DNA-binding protein"
/protein_id="AAB08486.1"
/db_xref="GI:455015"
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97.561
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1, .5349
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/db_xref="taxon:10090"
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                                                                                 Percent Identity:
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alignment_scores:
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KEYWORDS
                                        seq_documentation_block:
LOCUS AF006513
                                                                           seq_name: gb_pr:AF006513
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US-08-973-363-9 x A58683
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             ACCESSION
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Sequence 2 from Patent W09639505
A58683
            Homo sapiens CHD1 mRNA, AF006513
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1 (bases 1 to 153)
Griffiths, R. and Ti
AF006513.1 GI:2645428
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/db_xref="taxon:32644"
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US-08-973-363-9 x AF006513
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1 (bases 1 to 5947)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Characterization of the CHD family of proteins
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KLREBGHRVLIFSQMYMMLDILABYLKKÇOFPORLDGS KIGELKKALDHENABGSE
DCCFLLSTRAGGIGINLASADITVI FDSDWNPONDLQAQARAHRIGOKKQYNI YLVIY
KGSVEEDILERAKKKAVLDHLYLORMOTTGKTVLHTGARAPSSSTPRNEELSAILKFG
ABELFKEPEGEBOEDOEDDID DEILKARETHBNEDGPLTWODELLSQFKVANFSNNDED
DIELEPBROEDSOEDDID DEILKARETHBNEDGPLTWODELLSQFKVANFSNNDED
DIELEPBROEDSOEDDID DEILKARETHBNEDGPLTWODELLSQFKVANFSNNDED
DIELEPBROENSNWEEI I PEDOARRIEBEERQKELBEI YMLPRHRNCAKQI SFNGSEGR
RSRSRYGGSDSDS 13 BGK RFKKRGRPTI I PERNIKGF PARA I FRENK I SYKKEFGGPLE
RLDAJARDAELVUKSETDLARELGELVHAGCI KALKDSSGCTERTGGBLIGKVKGFFFRI
SGVQVNAKIV I SHEEBLI I PLHKS I PSID PEBRKQT I PGHTKAAHFDI INGKEDDSNLL
IGITEGYTGSBWAIKHDDIDLSTHHK ILPDDPDKKFDAKOLOTFAADVILKILLSRNDAK
LIGHTEGYTGSBWAIKHDDIDLSTHHK ILPDDPDKKFDAKOLOTFAADVILKILLSRNDAK
EALSGAGSSKRKARARKKNKAMKSIKVKEEETI LOWESTOFFERI
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EETIKQQNVRGMKKLDNYKKKOPETKRWIKNAS PEDVEYY NCOQELTDDLHKQYQIVG
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GLOKTIQTISFLNYLEHEBOLYGPETLVFPLSTITSWQREICTWASQONNAVYYLGDIN
SRNWIRTHEWTHHQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDS
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DDDEEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEEEEFETIER
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GLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
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KKQQQQQQQQQQHQASSNSGSEEDSSSSSEDSDDSSSEVKRKKHKDEDWQMSGSGSPSQS
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/db_xref="taxon:9606"
/chromosome="5"
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    from: 1 to: 5947
                                                                                                                                                                                              Percent Identity: 82.927
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                                                                                                                                                                                                   Quality: 166.00
Ratio: 4.256
Percent Similarity: 95.122
                                                                                            Align seg 1/1 to reverse of: ACO92372 from: 1 to: 101220
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26932 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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                         1 IleLeuProAspAspProAspLysLysProGlnalaLysGlnLeuGlnTh 17
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finishing Completed at Stanford Human Genome Center www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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gb_htg:AC021449
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Join
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
3 (bases 1 to 134355)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitsed (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitche
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134355)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 M. Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 M. Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267
Location/Qualifiers
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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4.256
95.122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CTD-2082I17"
                                                                                                                                                                                                                                                                                                                                                                                                                                      24497 c 25503 g 43951 t
                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                  Length: 41
Gaps: 1
Percent Identity: 82.927
                                                                                                                                                                                                                                     to: 134365
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                                                                                                    118346
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REFERENCE
AUTHORS
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ORGANISM
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LOCUS AC021449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Raderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, G., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Timper, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Vimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143079)
Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-58M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pieces.
AC021449
                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmer, A. and Zod
Direct Submission
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                                                                                                                                                  * as soon as it is available and * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Summary Statistics
sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L5154
Center clone name: 58_M_12
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                            1 38820: contig of 38820 bp in length
38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Zody, M.
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alignment_block:
US-08-973-363-9 x AC021449
seq_name: gb_htg:AC008531
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                                                                                                                                                                                                                                                                 Align seg 1/1 to: AC021449 from: 1 to: 143079
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                            116247 AAGCT.....CTTTCTGGTGCG 116263
                                                                                                                                                                                          116147 ATTCTTCCAGATGATCCCGATAAAAAAACCACAAGCAAAACAGTTGCAGAC 116196
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                                                                         34 luValGlnArgLeuThrGlyAla 41
                                                                                                                                                                                                              1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Ratio:
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51931 6261
62620 62719:
62720 7540
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43280 43379: gap of 100 bp
43380 46905: contig of 3526 bp in length
46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
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4.256
95.122
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47006. .51830
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26246 c 26678 g 45278 t
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92617. .106409
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 82.927
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Quality: 166.00

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REFERENCE
AUTHORS
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AUTHORS
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VERSION
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alignment_scores:
                                                                               ORIGIN
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LOCUS AC008531
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                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in 020 bases; pulse field gel estimation
Quality coverage: 6.4 in 020 bases; sum-of-contigs estimation.
*NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pleces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* This sequence will be replaced
* This sequence will be replaced
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Center clone name: CIT-HSPC_480B11
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Center: Joint Genome Institute
Center Code: JGI
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14565)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                               /clone="CTC-480B11"
/clone_lib="CalTech human BAC library C"
/26309 c 27580 g 48609 t 600 other
                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                   ocation.
                                                                                                                                                                                                                                                                                                             ssion number will be preserved.

56174: contig of 56174 bp in length
56274: gap of unknown length
100874: contig of 44600 bp in length
100874: contig of 44600 bp in length
100974: gap of unknown length
113127: contig of 12133 bp in length
113279: gap of unknown length
118190: contig of 4963 bp in length
118290: gap of unknown length
119584: contig of 1404 bp in length
119794: gap of unknown length
113287: contig of 1404 bp in length
123297: gap of unknown length
123397: gap of unknown length
14559: contig of 22262 bp in length.
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US-08-973-363-9 x AC008531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_htg:AC091946
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Percent Similarity:
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                                                                                                                                                                 Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 180259 bases at least Q30
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: RPCI-11_36012
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
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ne 5 clone RP11-36012, *** SEQUENCING IN
ig of 1358 bp in length of unknown length (1g of 1209 bp in length of unknown length ig of 1056 bp in length of unknown length
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31088 31087: gap of unkn
3666 3165: gap of unknow
36166 40978: contig of 48
40979 4563: contig of 456
45764 45763: gap of unknow
51346 51845: gap of unknow
51346 51845: gap of unknown
57460 67881: contig of 5514
57359: contig of 10422
67982 67991: gap of unknown le
74133 74232: gap of unknown le
74133 74232: gap of unknown le
79896 87511: contig of 6151 bp
79798 87611: gap of unknown length
92792 102794: contig of 57616 bp
12795 102804: gap of unknown length
967 110771: contig of 5903 bp in
1867 10966: contig of 9903 bp in
197 12378: contig of 6055 bp in
198 123888: gap of unknown length
199 123888: gap of unknown length
1103683: gap of unknown length
141644: gap of unknown length
16209: gap of unknown length
16209: gap of unknown length
16346: contig of 10861 bp in len
16346: contig of 1745 bp in len
                      Quality:
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  Ratio:
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/chromosome="5"
/clone="RP11-36012"
/clone_"RP11-36012"
/clone_lib="RPCI human BAC library 11"
/c35252 c 37061 g 60360 t 3202 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-JÜN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 1, 2001 this sequence version replaced gi:13677045. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195433 bp DNA linear PRI 01-JU1
Homo sapiens chromosome 5 clone CTC-428I11, complete sequence.
AC026778
AC026778.4 GI:14277282
                                                                                                                                                                                                                                                                                                                                                                    Quality: Phrap Quality >-40 99.9% of Sequence; Estimated Total Number of Errors is 0.2. STS Content: STS Content: WIT.13675 623101.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19433)

DDE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                    SHGC-58345 G38487
SHGC-103595 G57841.
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DOE Joint Genome Institute.
Direct Submission
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                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-428I11"
62762 a 37302 c 37040 g 58329 t
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                                                          Length: 41
Gaps: 1
Percent Identity: 82.927
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| Score_list:
| Strid Orig | Zscore | Escore | Len | Documentation |
| Silsil/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42754 | 197. (
| Silsil/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42751 | 197. (
| Silsil/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42751 | 197. (
| Silsil/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757 | 182. (
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| Silsil/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAA95280 | 129. (
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| Silsil/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AA60318 | 120. (
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Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
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Query: US-08-973-363-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters:
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-NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=GS08973363_eGG11_1 186 -NCPD=6 -ICPU=3 -LONGLOG
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US-08-973-363-9 x AAT42754
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 197.00
Ratio: 4.805
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAT42754 from: 1 to: 1316
                                                 1188
                                                                                                                                                                   1138 ATTTTACCTGATGATCCAGATAAGAAACCCCCAGGCTAAGCAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                              17 rargalaasptyleeullelysleuleansolysaspleulaarglysg
                                                                                                                                                                                                1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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Gaps: 0
Percent Identity: 95.122 Length:

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seq_documentation_block:
ID AAT42754 standard; cDNA; 1316 BP.
XX
AC AAT42754;

AC AAT42754;

XX
AC AAT42754;

XX

AC Chicken CHD-W gene (partial sequence continuation; chromodomain Helicase DNA binds GHD-W; chromodomain-Helicase DNA binds GHD-W; chromo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42754
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                                                                                                                                       The chicken CHD-W gene (ART42754) acting alone or in conjunction with the closely related CHD-IA gene (ART42751) Is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-IA gene as a probe The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-IA give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD^-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromodomain-helicase-DNA binding genes determine sex in
  - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.00 119.21 355.00 116.39 54.00 110.77 54.00 107.07 54.00 105.94
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389
802.
1.3
1.5
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luValGlnArgLeuThrGlyAla 41

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alignment_block: US-08-973-363-9 \times AAT42751
                                                                                                                                                                                                                                                                          alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                           Align seg 1/1 to: AAT42751
                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                 The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10·12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A - Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
4080 ATTTTACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avian
birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                    Sequence 6608 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken CHD-1A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT42751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1997
                        1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCACAGAGTTGCTGGTGCA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT4275:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex determination; chromodomain-Helicase-DNA binding chromodomain-Helicase-DNA binding on the W chromosor
                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-GB01341
                                                                                                                                                                                                              100.000
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                                                                                                                                                                                                                                 197.00
4.805
                                                                                                                                                                                                                                                                                                                                                  2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA; 6608 BP
                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                  1207 C;
                                                                                                                                                                                                            Percent
                                                                                             to: 6608
                                                                                                                                                                                                            Identity:
                                                                                                                                                                                                                                                                                                                                                  1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                 Length:
Gaps:
                                                                                                                                                                                                         41
0
95.122
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  4129
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17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG

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alignment_block:
US-08-973-363-9
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ID AAT42759 standard;
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                        Align seg 1/1
                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4130 CCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 4179
                                                                                                                                                                                           Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42751) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                             Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                      Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Great tit
                                                                                                                                                                    Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parus major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT42759;
                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW08149
                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 luValGlnArgLeuThrGlyAla 41
1 IleLeuProAspAspProAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                                                                                                           1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42759
                                                                                                                 Quality:
                                                                                                      Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHD-W
                         to:
                                                   x AAT42759
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                                                                                                                                                                                                                                                                                                                                                                                                                     Tiwari
                         AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-GB01341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                      191.00
4.659
80.392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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Gaps:
Identity:
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                           153
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1
80.392
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alignment_scores:
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                                                                   Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination; chromodomain Helicase DNA binding CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 Ala 41
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 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 52..81
182.00
4.439
                                                                                                                                                                                                                                                                                                                                                                            "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                                  <u>و</u>;
                                                  24 T; 0 other;
Length:
Gaps:
  51
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amino
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seq_documentation_block:
ID AAT42758 standard; DNA; 153 BP
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US-08-973-363-9 x AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42758
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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759): Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-14 (see also AAT42751) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine birds - used for sex determn. and to control sex of prog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                           Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                           WPI; 1997-043127/04.
P-PSDB; AAW08148.
                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                               (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                        06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AATTACTGAATAAAGACCTTGCAAGAAAGGAAGGCACAAAGGCTTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IleLeuProAspAspProAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATTITACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysLeuLeuAsnLysAspLeuAlaArgLysGluValGlnArgLeuThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp.
                                                                                                                                                                                                                   Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                        95GB-0011439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome;
                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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amino
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Soxco

Sequence 153

вP;

56 A;

36

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31

<u>و</u>;

30 T; 0

other;

foetus etc.

and

to manipulate the sex of progeny.

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PXXXX 
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ID AAT42756 standard; DNA; 153
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US-08-973-363-9 x AAT42758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; :
                                                                                 Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
     Claim
                                                                                                                                                                           WPI; 1997-043127/04.
                                                                                                                                                                                                                            Griffiths R,
                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse CHD-1 gene (bases 3855-977).
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                                                                                                                                              P-PSDB; AAW08146
                                                                                                                                                                                                                                                                                   (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTACCTGATGATCCAGATAAGAAACCCCCAGGCTAAGCAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex determination; chromodomain-Helicase-DNA binding
; CHD-W; W chromosome; ss.
                                                 chromodomain-helicase-DNA binding genes determine sex — used for sex determn. and to control sex of progeny
     8
Fig 3; 76pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                               Tiwari
                                                                                                                                                                                                                                                                                                                                          95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                 96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182.00
4.439
80.392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from:
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Gaps: 1
Percent Identity: 76.471
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6
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amino
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seq_documentation_block:
ID AAV59280 standard; cDNA; 1:
XX
AC AAV59280;
XX
DT 14-DEC-1998 (first entry)
XX
DE Altered telomere repeat bir
XX
ds; human; telomere repeat kW
telomere; ageing; ataxia te
XX
OS Homo sapiens.
OS Synthetic.
XX
OS Homo sapiens.
Y**
OS Homo sapiens.
Y**
OS Homo sapiens.
Y**
OS Ynthetic.
XX
OS Homo sapiens.
XX
OS Homo sapiens.
Y**
OS Homo sapiens.
OS Homo sapiens.
Y**
OS Homo sapiens.
OS Homo sa
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US-08-973-363-9 x AAT42756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW4827549. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AACTACTTAGCAGAGATCTTGCAAAAAGAGAGGCTCAGAGACTTTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 153 BP; 61 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 ysLeuLeuAsnLysAspLeuAlaArgLysGluValGlnArgLeuThrGly 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
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                                                                                                   98US-0018628
97US-0800264
                                                                                                                                                                                                   98WO-US02765
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/product= "A-TRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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4.175
78.431
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
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1
68.627
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seq_documentation_block:
ID AAK88882 standard; cDNA; 421 BP
XX
AC AAK88882;
XX
O5-NOV-2001 (first entry)
XX
Human digestive system antigen
XX
Human; digestive system antigen
XX
Human; digestive system disorder; Meck
XX
digestive system disorder; Meck
XX
MO200155314-A2.
XX
PPN W0200155314-A2.
XX
PP 17-JAN-2001; 2001WO-US01324.
XX
PF 17-JAN-2000; 2000US-0180658.
PR 04-FEB-2000; 2000US-0180658.
PR 04-FEB-2000; 2000US-0180658.
PR 04-FEB-2000; 2000US-0180658.
PR 16-MAR-2000; 2000US-0180654.
PR 16-MAR-2000; 2000US-0180674.
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US-08-973-363-9 x AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
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Ratio: 5.160
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAV59280 from: 1 to: 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeitasia, Down's syndrome, atmophy of the skin, age-related macular degeneration, atheroscierosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                        Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                               Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
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Gaps: 0
Percent Identity: 100.000
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     18-AUG-2000)
22-AUG-2000)
22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
30-AUG-2000)
31-SEP-2000)
01-SEP-2000)
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29-SEP-2000

20-CCT-2000

02-CCT-2000

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02-CCT-2000
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18-APR-2000;
19-MAY-2000;
               2000US-023208

2000US-0231968

2000US-0231968

2000US-0232397

2000US-0232399

2000US-0232400

2000US-0233063

2000US-0233063

2000US-0233063

2000US-0233063

2000US-0234223

2000US-0234223

2000US-0234274

2000US-0234274

2000US-0234274

2000US-0234284

2000US-0234884

2000US-02358484

2000US-0235836

2000US-0236367

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2000US-0236367

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2000US-0236370

2000US-0237037038
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2000US-0227182
2000US-0227109
2000US-0229287
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2000US-0229359
2000US-0229513
2000US-023950
2000US-0239513
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2000US-0198123
2000US-0205515
2000US-0209467
2000US-0214886
2000US-0215135
2000US-0216840
2000US-021647
2000US-0216880
2000US-0217487
2000US-0217487
2000US-0217496
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13-0CT-2000
20-0CT-2000
20-0CT
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08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
17-NOV
The present invention provides the protein and coding sequences
                                                     Claim
                                                                                                 Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                          2001-502630/55.
                                                                                                                                                                                                                                                                                               CA,
                                                  1;
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                                                     SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                 2000US-024929

2000US-0241785

2000US-0241785

2000US-0241786

2000US-0241808

2000US-0241808

2000US-0246474

2000US-0246475

2000US-0246476

2000US-0246476

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2000US-0249216

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2000US-02511989

2000US-02511989

2000US-02511989

2000US-02511989

2000US-0251097
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                                                  NO 1198;
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                                            986pp; English.
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US-08-973-363-9 x
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive
                                                                                                                                                                                                                                                                                                                                              Human colorectal cancer antigen cDNA
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2000US-0189874.
2000US-0189123.
2000US-0198123.
2000US-029467.
2000US-029467.
2000US-0214886.
2000US-0215135.
2000US-0216880.
2000US-0217487.
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2000US-0225214 2000US-0225266

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alignment_block:
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08-NOV-2000;

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08-NOV-2000;

17-NOV-2000;
                                                                                                                                The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAI57647 AAI57649 and AAM35649 AM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                    Isolated polypeptide disorders related to and also for testing
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DB; AAM38625.
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                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
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11-JUL-2000;
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PR 23-MAR-2000; 2000US-
PR 11-JUL-2000; 2000US-
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PI Venter JC, Adams M,
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seq_documentation_block:
ID AAA95315 standard; DNA; 2595 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a number of methods which can be used to detect the presence of bovine Neospora infection. The infection leads to neosporosis in cattle, and can cause abortion of foetuses. The present sequence comprises a vector coding sequence. The sequence, and the protein it encodes, can also be used to produce vaccines against the infection and in protein isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2595 BP; 609 A; 796 C; 637 G; 553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 71-72; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W0200057905-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neospora sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA95315;
                                                                                                                                                         328 CCACAAGATCCAGACCGGAGTCTCAAGTATCCTGTACGGCTGCTGATTGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2000; 2000WO-US08180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nss-IRNA coding sequence; aborted bovine foetus; bovine neosporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neospora NC-p65 vector coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel immunodominant Neospora antigens, N94 and N97, useful for protecting bovine neospora and greatection by bovine Neospora and detecting the presence of antibodies specifically immunoreactive with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB26153
                                   378 AGACAAGCCTGCGGGGGATGAAGAGGAGACTAGACCATCATTTGTGCAGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neospora antigens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
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                                                                                         9 ....LysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
                                                                                                                                                                                                    3 ProAspAspProAspLys.....
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Ratio:
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2.067
60.000
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alignment_block:
US-08-973-363-9 x AAX39679
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                                                                                         Percent Similarity:
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Ratio:

61.50 2.278 75.000

Gaps: 1 Percent Identity: 33.333

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seq_documentation_block:
ID AAX39679 standard;
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                                         The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                   New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 CGGCACTACATTCGGAGCTTGCACAACGCGTTGTGAAAGAGCTAAATGGG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX39679;
Sequence 2911 BP; 957 A; 519 C; 686 G; 749 T; 0 other;
                               lung cancer.
                                                                                                                                                                                                                                                                                     Claim 67; Page 496-497; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1998;
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97US-0061765.
97US-0948705.
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Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0896164
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Scanlan MJ,
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, Stockert E;
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alignment_scores:
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  Percent Similarity:
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                                                                                                                     AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                                                                                                                                                                                                                                                                                        Novel nucleic acids, used to develop products for the diagnosis treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer .
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                                                                                                           dysplasia or hyperplasia.
                                                                                                                                                                                                                                                              Claim 15; Page 393; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Schlegel
                                                                                                                                                                                                                                                                                                                                                                                        Endege WO,
Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; sarcoma; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression product; diagnosis; tumour; colon cancer;
colorectal adenocarcinoma; cell line SW480; cell proliferation;
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                WPI; 2000-087220/07
                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnThrAr 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer
                            Quality:
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                                                                                   673 BP;
              Ratio:
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Catino TJ,
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60.50
2.161
75.676
                                                                                 218 A; 139 C;
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                                                                                                                                                                                                                                                                                                                                                                                       KE, Astle
Derti A,
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Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasia; dysplasia;
                            Length:
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d DM, Lewis
                                                                                 142 T;
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 29.730
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                                                                                 other;
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                                                                                                                                                                                                                                                                                                                                                                                                     Bushnell SE;
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seq_documentation_block:
ID ABI99578 standard;
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US-08-973-363-9 x AAZ80575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                          expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence
                                                                                                                         genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57314) or by determining the
                                                                                                                                                                                                                                                                          Claim 2;
                                                                                                                                                                                                                                                                                                          genes
                                                                                                                                                                                                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 GTTTGAGAACCTCTGCAAAATCATG...AAAGACATATTGGAGAAAAAAG
                                                                                                                                                                                                                         The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular
                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200188188-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABI99578;
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                                which are
                                                                                                                                                                                                                                                                                                                                                                                                                       Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001; 2001WO-JP04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse ischaemic condition related cDNA sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ischaemia;
                                                                                                                                                                                                                                                                        Page 1516-1517; 2690pp; English
                                used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischaemia;
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                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compressive ischaemia;
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                                exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischaemic condition; ischaemic disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occlusive ischaemia;
                                               condition related sequence,
                              present invention
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Sequence 826 BP;

270 A;

161 C;

206 G;

189 T;

0 other

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Query length: 41
Database: EST: *
Database: eguences: 13736207
Database length: -1841457050
Search time (sec): 4390.400000
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Query: US-08-973-363-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ş
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gb_est1:AL659353
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-Q-/cgn2_L/USPT0_spool/US08973363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST -OpmT-fasta_ -SUFFIX-p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH-0.100 -LOOPEL-0.000 -LOOPEXT=0.000 -GAPOP-4.500
-GGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.000 -GAPOP-6.000
-FGAPEXT=7.000 -YGAPOP-10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP-10.000 -YGAPOXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOX=10 -MARRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN-200 -THE_COORS-pct -THE_MAX=100 -THE_MIN=0
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-NCPU=6 -LOPU-3 -LONGLOG -DEV_TIMEOUT=120 -MARR_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of: US-08-973-363-9 to: EST:*
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                   | ALI32212 Tetraodon nigroviridis | ALI32335 Tetraodon nigroviridis | ALI23335 Tetraodon nigroviridis | ALI23335 Tetraodon nigroviridis | ALI233103 Tetraodon nigroviridis | ALI18979 Tetraodon nigroviridis | ALI18979 Tetraodon nigroviridis | ALI33703 Tetraodon nigroviridis | ALI33703 Tetraodon nigroviridis | ALI392041 Tetraodon nigroviridis | ALI39249 Tetraodon nigroviridis | ALI34289 Tetraodon nigroviridis | ALI34288 Tetraodon nigroviridis | ALI34288 Tetraodon nigroviridis | ALI317122 Tetraodon nigroviridis | ALI317123 Tetraodon nigroviridis | ALI317123 Tetraodon nigroviridis | ALI317123 Tetraodon nigroviridis | ALI317128 Tetraodon nigroviridis | ALI317128 Tetraodon nigroviridis | ALI317128 Tetraodon nigroviridis | ALI31888 Tetraodon nigroviridis | ALI31888 Tetraodon nigroviridis | ALI31888 Tetraodon nigroviridis | ALI3195138 Tetraodon nigroviridis | ALI317128 Tetraodon nigroviridis | ALI317128 Tetraodon nigroviridis | ALI31728 Tetraodon nigroviridis | ALI3175138 Tetraodon nigroviridis | ALI3175188 Tetraodon nigroviridis | ALI3175188 Tetraodon nigroviridis | ALI3175188 Tetraodon nigroviridis | ALI3175188 Tetraodon nigroviridis | ALI31888 Tetraodon nigroviridis | A
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BF239967 601905170F1 NIH_MGC_5;
AM996787 QV3-BN0047-230200-102
AM997058 QV3-BN0047-150400-152
AL293839 Tetraodon nigrovirid;
AL352864 Tetraodon nigrovirid
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AUTHORS
TITLE
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VERSION
KEYWORDS
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ORIGIN
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Percent Similarity:
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gb_est2:H53564
gb_est2:BG757172
gb_est1:AW364689
gb_est1:AL658477
gb_gss:CNS03IQ2
seq_name: gb_est1:AL644594
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US-08-973-363-9 x AL659353/rev
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LOCUS AL659353
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                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: AL659353 from: 1 to: 593
                                         246 AAGCACAAAGACTTTCT 230
                                                                                                                       296 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG
                                                                                                                                                                                                       34 luValGlnArgLeuThr 39
                                                                                                                                                                                                                             1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TRODICALIE_EEQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 593)

Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        western clawed frog.
Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Huckle E
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AL659353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Organism="Silurana tropicalis"
//db_xref="taxon:8364"
/clone="Theu045e20"
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/lab_host="Escherichia coli DH10B"
/lab_host="Nector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
vas oligo dT primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
a 134 c 114 g 226 t
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4.816
97.436
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! BG757172 602710541Fl NIH_MGC.
! AW364689 PM3-D70037-231299-0
! AL658477 AL658477 XGC-neurul
! AL245891 Tetraodon nigroviri
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SOURCE
ORGANISM
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US-08-973-363-9 x AL644594
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LOCUS AL644
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                                                                                                                   seq_documentation_block:
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                                 ACCESSION
                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                             456
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                                                                                                                                                                                                                   luValGlnArgLeuThr 39
                                                                                                                                                                                                                                                                      IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                          CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG
                                                                                                                                                                                      AAGCACAAAGACTTTCT
                                                                                                                                                                                                                                                                                                                           gb_est1:BB155356
                          BB155356 RIKEN full-length enriched, 16 days neonate thymn musculus cDNA clone A130024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinxton, Cambridgeshire, CB10 1SA, Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       western clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
BB155356.2
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
125 c 156 g 141 t 1 others
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4.816
97.436
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/dev_stage="egg"
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/clone="L1E1d12"
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L1E1d12 5', mRNA
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Harakawa,T., Carninci,P., Fukuda,S., Furuno,M., Komo,H., K., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., K., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Sano,H., Sano,H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RİKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Su,Y. and Hayashizaki,Y.
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wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Zanaka,T., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                            prepared by using trehalose thermo-activated transcriptase and subsequently enriched for
                                                                                                                                                                                                                            Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                        prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="thymus"
/dev_stage="16 days neonate"
/lab_host="9H10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thymus'
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/clone="A130024L16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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I., Kouda
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Elekaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

La (bases 1 to 660)

RS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Miramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki

D., Shibata, K., Shinagawa, A., Tshiraki, T., Sogabe, Y., Suzuki, H.,

Tagani, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, Y. et al. 2001)

Muramatsu, M. and Hayashizaki, Y. et al. 2001

On Jul 21, 2000 this sequence version replaced gi:9356558.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9216

Fax: 81-45-503-9216
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BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
Bmail: genome-res@gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2007)
genes. Genome Res. 10 (10), 1617-1630 (2007)
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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

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alignment_block:
US-08-973-363-9 x BB461065
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA, library was prepared and sequenced in Mouse Genome CDNA, library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken.

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

DIVISION OF Experimental Animal Research in Riken contributed to
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Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
Sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
Konno,H., Fukunshi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Computational Analysis of Full-Length Mouse cDNAs Compared with Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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/lab_host="pH10B"
/lab_host="pH10B"
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/note="Sciences Center and Genome Encyclopedia
/note="Site_1: Sciences Center and CDNA was
/note="Site_1: Sciences Center and CDNA was
/note="Site_1: Spinal ganglion"
/note="Site_1: Spinal ganglion"
/note="Site_1: Sal1; Site_2: Spinal Research in Riken
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/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal ganglion"
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                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wag1,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
uavashiayi v
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930033J21 3', mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                  /tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
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                                                                                                                                                                                                                                                                                                                           Email: genome resegsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Isikawa,T., Ozawa,K., Tanaka,T., Matsuu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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Jyg-MC(B) cDNA
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary 10 (11), 1757-1771 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                    Konno, H., Fukunishi, Y.,
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKTZ); Email s. wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
sraunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp31371040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 430)
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Contact: Bloecker
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/tissue_type="nammary gland"
/ceil_line="RCB-0527 Jyg-Mc(B)"
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/db_xref="taxon:10090"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Dk72p3131040"
/clone_lib="313 (synonym: hlcc2)"
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Li Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Capabs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.linl.gov/bbrp/image/image.html

Insert Length: 1924 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 418.
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1 (Dases 1 to 547)
1 (NGI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
1 NGI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
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/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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95.122
                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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        /note="Organ:
Site_2: NotI;
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Gaps: 1
Percent Identity: 82.927
uterus; Vector: pCMV-SPORT6; Site_1: SalI; Cloned unidirectionally. Primer: Oligo dT
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                                                                                                                                                                                                          Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                 Saito,K., Yamamoto,J., Nak
,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 866)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto,
Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
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   precursor cells"
149 c 196 ~
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/clone_lib="NT2RM4"
                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAM9753 row: h column: 16
High quality sequence stop: 488.
Location/Qualifiers
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1028)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                              387
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/tissue_type="melanotic melanoma"
/lab_host="DHINDB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Si
Site_2: Sall; Cloned unidirectionally. Pri
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                                                                                                                    Percent Similarity:
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AL280261.1 GI:8024707
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Acanthopterygii; Tetraodontiformes;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Charaterization and repeat analysis of the compact genome of the Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
scale clone-end sequencing project of the Tetraodon at genome. For more information, please take a look at
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 856)
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="103K08"
/clone="10="G"
/clone=lib="G"
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/note="Genoscope Sequence ID : C0BG103BF04LP1-end : T7"
/note="Genoscope Sequence ID : C0BG103BF04LP1-end : T7"
                                                                                                                                   150.00
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89.744
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LOCUS BF239967
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alignment_block:
US-08-973-363-9 x BF239967
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1 (bases 1 to 821)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lnage.lnl.gov plate: LLCM1033 row: k column: 18
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
//dlone=]ib="NHRGE:4133129"
//clone=]ib="NHRGE:4133129"
//clone=]ib="NHRGE:4133129"
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//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glonte RNA);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glontech);
//note="Organ: bone marro
                                                                                                                  139.00
4.088
94.444
                                                                                               Length: 36
Gaps: 1
Percent Identity: 80.556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simpson, A.J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QV3-BN0047-230200-102-d03 BN0047 Homo sapiens
                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.ludwig.org.br/scripts/gethtm12.p1?t1=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
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                      Ratio:
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Location/Qualifiers
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                                                                                                                         profiles into the pUC 18 vector. Neverther tissue mRNA and CDNA amplification were performed low stringency conditions."

a 59 c 72 g 123 t
                                                                                                                                                                                                    Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
  129.50
3.924
94.286
                                                                                                                                                                                                                                                                                     /note="Organ:
                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                             /clone_lib="BN0047"
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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E., Garcia Correa, R., Verjovski-Almeida, S., Cos
  Percent Identity:
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: +55-11-2707001
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as Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
as Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Costa,F.F., u
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                                                            tissue mRNA and cDNA amplification were performed under low stringency conditions."
154 c 126 g 241 t
                                                                                                                                                                                                                                                                              /note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-973-363-9 x AW997058/rev
alignment_block:
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                                                                                                                                                                                                                alignment_scores:
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Ratio: 3.818
Percent Similarity: 100.000
                                                                                        Percent Similarity:
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                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1047)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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1 (bases 1 to 1047)

1 (bases 1 to 1047)

Roest-Crollius; H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
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GSS: genome survey sequence.
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Tetraodon nigroviridis
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365 AG...CAGTCCCAKACAGGA 349

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Search information block:
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Query ! Europth: 88
Database: GenEmbl:*
Database: length: 1873333701
Search time (sec): 4907.710000
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9b_pt:AC060899

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9b_rt:C:AL589701
9b_htg:AL545746
9b_htg:AL545746
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-O-/cgn2_1/USPTO_Spool_US08973363/runat_01082002_080050_18581/app_query.fasta_1.638
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-DEV_TIMEOUT-120 -MARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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365 'AC012624 Homo sapiens chrome
436 AC09446 Homo sapiens chrome
437 AC09531 Homo sapiens chrome
438 AC025121 Homo sapiens chrome
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431 AC02578 Homo sapiens chrome
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434 AC03338 Homo sapiens chrome
435 AC025121 Homo sapiens chrome
436 AL589701 Mouse DNA sequence
437 AF064864 Homo sapiens chrome
438 AC05370 Alcelaphine herpesv
438 AC05370 Alcelaphine herpesv
439 AF165176 Homo sapiens chrome
445 AL58926 Mus musculus chrome
446 AC05878 Homo sapiens chrome
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448 AC0173609 Mus musculus chrome
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445 AC09878 Homo sapiens chrome
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4476 AC099077 Mus musculus chrome
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450 AL60525 Mouse DNA sequence
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Griffiths,R. and Korn,R.M.
A CHDI gene is Z chromosome linked in the chicken Gallus domesticuene 197 (1-2), 225-229 (1997)
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"gene="CHD-Z"
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
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/translation="MNGHSDEESYRNSSGESSRSDDDSGSASGSGSGSSSSGSSSDGSS
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THVIRNPDVERLKETTNHDDSSRDSYSSDHLSQYHDHHKDRHQDAYKKSDSRKRPY
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                                                          Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
                                                                                                                                                                                           Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 ND Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                              Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US. 3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 101220)
DOE Joint Genome Institute
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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4.909
98.876
/organism="Homo sapiens"
/db_xref="taxon:9606"
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LOCUS AC012624
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Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624
AC012624.6 GI:14993679
Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                      Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
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                                                                                                  Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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/clone="RP11-58M12"
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LOCUS AC021449
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAreilano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McReus, L., Morrow, J., Naylor, J., McRensan, R., McBers, R., McBers, R., McBers, R., McGurk, A., McKernan, K., McPheeters, R., Melfarin, J., Meneus, L., Morrow, J., Naylor, J., Nayl
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Homo sapiens clone RP11-58w12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-58M12
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AC021449.3 GI:10047806
HTGS_PHASE1; HTGS_DRAFT.
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Mammalia; Eutheria; Primates; Catarrhni; Hominidae; Homo.
1 (bases 1 to 143079)
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a 24497 c 25503 g
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/db_xref="taxon:9606"
/chromosome="5"
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CE, 10 unordered
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Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,

Zimmer, A. and Zody, M.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38820: contig of 38820 bp in length
38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511: gap of 100 bp
40512 43279: contig of 2768 bp in length
43280 43799: gap of 100 bp
43380 46905: contig of 3526 bp in length
43380 46905: contig of 3526 bp in length
47006 51830: contig of 4825 bp in length
51831 51930: gap of 100 bp
51831 562619: contig of 10689 bp in length
51831 562619: contig of 10689 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.6 in Q20 bases; Quality coverage: 4.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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106510 14307
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62720 75408: contig of 12689 bp in length
75409 75508: gap of 100 bp
75509 92516: contig of 17008 bp in length
92517 92616: gap of 100 bp
92617 106409: contig of 13793 bp in length
                                                                                                            vector_side:left"
                                                                                                                                            clone_end:SP6
                                                                                       38921.
                                                                                                                                                              /note="assembly_fragment
                                                                                                                                                                                                                                                        /db_xref="taxon:960
/clone="RP11-58M12"
                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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/note="assembly_fragment"
                                                    note="assembly_fragment"
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AUTHORS

DOE Joint Genome Institute

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REFERENCE
AUTHORS
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                                                                                                                                                                                                             seq_documentation_block:
LOCUS AC008531
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 REFERENCE
                                                                                                                                    KEYWORDS
                                                                                                                                                VERSION
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                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                       seq_name: gb_htg:AC008531
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              JOURNAL
                               TITLE
                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                            AC008531 145659 bp
Homo sapiens chromosome 5 clone
                            Sequencing of Human Chromosome
                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                      Homo sapiens
                                                                                                                                 HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                AC008531.3 GI:12830078
                                                                                                                                                                  AC00853
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                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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DRAFT SEQUENCE,
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BASE COUNT
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US-08-973-363-11 x AC008531
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Source
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48336 AGACAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 48385
                                                                                                                48286 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG 48335
                                     17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
                                                                                                                                                  1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in 020 bases; pulse field gel estimation
Quality coverage: 6.4 in 020 bases; pulse field gel estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pleces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the arcession number will be preserved.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.
------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
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56275
100875
100975
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118291
1119695
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4.395
92.045
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/db_wref="haxon:9606"
/chromosome="5"
/clone="CTC-480B11"
/clone="CTC-480B11"
/clone=1th="calfech human BAC library C"
/clone_1th="calfech human BAC 1600 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ssion number will be preserved.
56174: contig of 56174 bp in length
56274: gap of unknown length
100874: contig of 44600 bp in length
100874: contig of 44600 bp in length
100974: gap of unknown length
113127: contig of 12153 bp in length
11329: gap of unknown length
118190: contig of 4963 bp in length
118290: gap of unknown length
118290: gap of unknown length
119594: contig of 1404 bp in length
123397: gap of unknown length
123397: contig of 3503 bp in length
123397: gap of unknown length
13559: contig of 22262 bp in length.
                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                 Length: 88
Gaps: 0
Percent Identity: 78.409
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REFERENCE
AUTHORS
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Homo sapiens chromosome 5 clone Rp11-36012,
PROGRESS ***, 33 unordered pieces.
AC091946
AC091946.1 GI:14333882
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Estimated insert size: 20450; agarose-fp estimation
Batimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 31 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
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Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Sequence (19-JUN-2001) Production Facility (19-JUN-2001) Produ
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Center Project Name: 544799
Center clone name: RPCI-11_36012
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Web site: http://www.jgi.doe.gov
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DOE Joint Genome Institute.
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8: contig of 1358 bp in length
8: gap of unknown length
7: contig of 1209 bp in length
7: gap of unknown length
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0: gap of unknown length
0: gap of unknown length
4: gap of unknown length
4: contig of 1474 bp in length
4: gap of unknown length
5: contig of 1502 bp in length
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                                                                                                                                                                                                                www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of
Estimated Total Number of Errors is
                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                 Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACUZZIZI 219258 bp DNA linear PRI 30-AUG-
Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
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     Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu wality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.4.
STS Content:
                                                                                                                                            Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USS 1 (bases 1 to 219258)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
------Genome Center
Center: Joint Genome Institute
Center: Code: JGI
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SHGC-103595 G57841
                                                                                                                                            2 (bases 1 to 276181)
DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 276181)
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WI-13675 G23101
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/chromosome="5"
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Gaps: 0
Percent Identity: 78.409
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Consensus quality: 229677 bases at least Q40
Consensus quality: 256163 bases at least Q30
Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 260799 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Quality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project Information
Center Project Name: 435334
Center clone name: RPCI-11_75H1
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-75H1"
/clone_lib="RPCI human BA(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL Submitted (30-AN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:17384104.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mi3 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT: Tr:, TREMEL; Mp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-202F3 is
from the RPC1-23 Mouse PAC Library
constructed by the group of Pleter de Jong.

PECTOR: pBACe3 6

The Cather details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL589701.9 GI:18476660
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                                                                                                                                                                                                                                                                                                                                                                      OR: pBACe3.6

sequence is the entire insert of clone RP23-202F3 The true end of clone RP23-171015 is at 179956 in this sequence. The right end of clone RP23-153B6 is at 117857 in this sequence. Location/Qualifiers
                  /note="Single clone region. Sequence from clone PCR only." 29783. 30099
/note-"Single clone region. Sequence from reads from a short insert library derived from a clone PCR. Restriction digest data confirm the assembly." a 46953 c 46966 g 61646 t
                                                                                                                                                                                       /clone_lib="RPCI-23"
3942. .4127
                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="13"
                                                                                                                                                                                                                                            /clone="RP23-202F3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_htg:AL645746
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US-08-973-363-11 x AL589701/rev
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LOCUS AL645746
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Ratio: 2.961
Percent Similarity: 81.013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LeuLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSe 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 eGlyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
                                                                       Direct Submission Submitted (11-7AN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 28, 2001 this sequence version replaced g1:17017892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL645746 282611 bp DNA linear HTG 12-C
Mus musculus chromosome 13 clone RP23-153B6, *** SEQUENCING
PROGRESS ***, in unordered pieces.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: mouseg@har.mrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: UK Medical Research Council Center code: UK-MRC
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
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Percent Identity: 55.696
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                                                                                                         sum-of-contigs Quality
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SEQUENCING HTG

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10-JAN-2002

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alignment_block:
US-08-973-363-11 x AL645746
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Quality:
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ORIGIN
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Percent Similarity:
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                      gb_htg:AL645990
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fragment_chain:1"
71289. .219059
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57461. .6
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51151. .
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fragment_chain:2"
219160. .250487
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2.961
81.013
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/note="assembly_fragment:05089"
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fragment_chain:1"
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60936 c 60357 g 80189 t
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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/chromosome="13"
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Gaps: 3
Percent Identity: 55.696
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LOCUS AL645990
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TITLE
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 201289 bases at least Q40
Consensus quality: 201587 bases at least Q30
Consensus quality: 201880 bases at least Q20
Insert size: 202406; sum-of-configs
Insert size: 202406; sum-of-configs
Quality coverage: 13.87x in Q20 bases; sum-of-configs
Coverage: 13.39x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 11, 2002 this sequence version replaced gi:17529594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Mammalia; Eutheria;
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                                        /note="assembly_fragment:00114" 118497. .126220
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                                                                                                                                                      /note="assembly_fragment:00235
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fragment_chain:1"
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                                                                                            /note="assembly_fragment:02210
fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1
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/chromosome="11"
    /note="assembly_fragment:05423.0"
126321. .130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-23"
1. .2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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seq_documentation_block:
LOCUS A58694
DEFINITION Sequence 13 fr
ACCESSION A58694
VERSION A58694 1 GI:3
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US-08-973-363-11 x AL645990/rev
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Ratio: 2.791
Percent Similarity: 80.723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LysH1sLeuH1sLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
                                                                                                Patent: WO 9639505-A 13 12-DEC-1996; ISIS INNOVATION (GB) Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                   137 bp
Sequence 13 from Patent WO9639505.
A58694
                                                                                                                                                                                 1 (bases 1 to 137)
Griffiths, R, and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                      unidentified.
                                                                                                                                                                                                                                                                                                                             A58694.1 GI:3714252
                                                                                                                                                                                                                                              inclassified
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    76
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fragment_chain:3"
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fragment_chain:3
clone_end:SP6
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10 c 33 g 18
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44361 c 43131 g
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fragment_chain:3"
135999. .180011
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fragment_chain:3"
130813. .135898
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fragment_chain:3"
180112. .189518
                                                                Location/Qualifiers
1. .137
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MEDLINE
REFERENCE
AUTHORS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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ACCESSION
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Quality:
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LOCUS
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US-08-973-363-11 x A58694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: A58694 from: 1 to: 137
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                                                                               polyA_signal
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                                                                                                                                      polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ysGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAla 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGlu.L 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensser,A., Pflanz,R. and Fleckenstein,B. Direct Submission Submitted (27-MAY-1997) Institut fuer Klinische und Molekulare Virologie, Friedrich-Alexander-Universitaet Erlangen-Nuernberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 130608)
Ensser,A., pflanz,R. and Fleckenstein,B.
Primary structure of the alcelaphine herpesvirus 1 genome
J. Virol. 71 (9), 6517-6525 (1997)
97404659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wildebeest herpesvirus.
Alcelaphine herpesvirus 1
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schlossgarten 4, Erlangen 91054, Germany Location/Qualifiers
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4.390
89.130
                                                         /evidence=not_experimental complement(1300. .1305) complement(1300. .1305) complement(john(1796. .2230,2313. .2477)) complement(john(1796. .2230,2313. .2477)) note="spliced cDNA detected by 5'RACE-PCR"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Alcelaphine herpesvirus 1"
/strain="C500"
                                        /codon_start=1
                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                     'note="putative ORF"
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VRL 19-0CT-2001

alignment_scores:

BASE COUNT

misc_feature misc_feature misc_feature misc_feature

COMMENT FEATURES

REFERENCE

ORGANISM

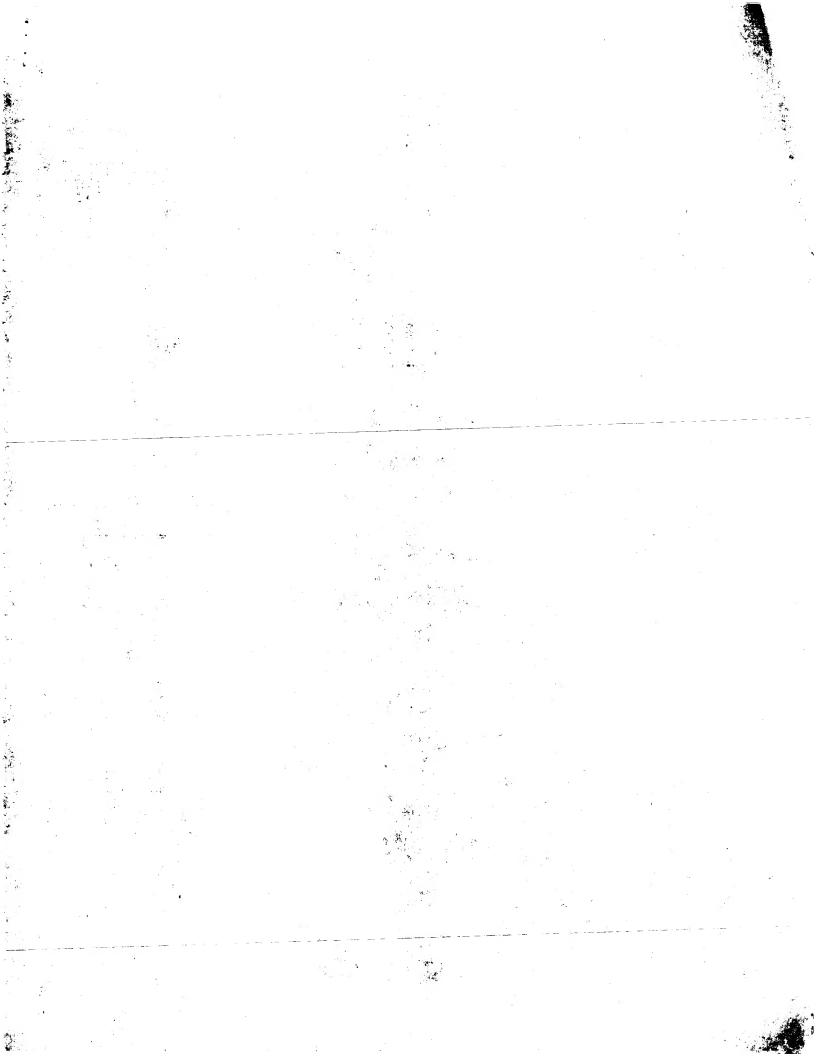
AUTHORS TITLE

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DRCGNGHIAQQPGVGPPDIPLCDFSVTVHNLVDGDIREGMESVPRVMAADMRVARRLI
ETQYSTPGLDITDATLANNLGLTYHIPSEHQVTVESKKYDCIGIGEKTTFTQRDDLI
GTILAIVESCTNCILGPVENYEEFLIGLSISVPEGIHYRHEVNSIMAMAKDFCSSMNF
GFQVNSAENGNCLLRSVVATANAPCVVPGPSLKPYFKKPGSAILRVNLHTEHFLSGGI
CCMASGIGASETFTPTPSQLRNLLQFNLIVKAENLALSGHDVSDGGLICAVCEMMFAG
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AVTDSEIFRIPYTHVVRFIDRWEIRVRKPDVGFHGSRGVRFRGHGAAVMCSTLASTI
GATGCLOKGMITTSFISOFTLOGLGIITERMCGWGOQELSATATOMLTKY ANTYLEAFAK
TLNYAGVPLVQGFVTLSPTLREKRAMAFTGSLSITGLPPYILKPPTAETLDAAMERNR
QLLLVEVGYPDYGKGKLHNPVNIMNSESGRHAHILHQALQCLMI ITPFGKVIHLCODW
QYMEKYTMFKIAKAGCGUGLGLMSASFLPAHTLRLLKKWHERNLMYNHRIIKNSMLKVD
QYMEKYTMFKIAKAGCGUGLGLMSASFLPAHTLRLLKKWHERNLMYNHRIIKNSMLKVD
SAAALVVIADNEYQDVSKKMDIALSGWGCPFHILGNLTPNSNTIVISDKNQYGEIVDI
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LTTIKGTIHIYVRYEDSNSTTALNILEINPFQKFAPIGVILDNUKLKLYVNSEMEDHY
EVPLDLCSVYGNDCFSGFMSRDPLCTTYYNNTCSFKAPIGVETGGPANRTIESEMCGBUY
APTVVKHQVSIPLLSNSYLSCPAVSNHADYFWTKDGFTEKRCHVKTHKNDCILLIANS
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LSGSHKFRRIAGQVELYTSDTAMHRPQFVQATAVHKNESYDDKIYFFFQENSHSDFKQ
FPHTVPRVGQVCSSDQGGESSLSVYKWTTFLKARLACVDYDTGRIYNELQDIFIWQAP
                                                                                                                                                                                                                                               DTFTVEHQNTQLLSVPVSRLKHNWTLFSKSVDLLYVKEDQVLPEETSYGNTEVHLTVD
PYSIISQSTTRPNVLYHLLPGGGYEDALLALITNSGSPDTVVYPGGKYRHNRREDAA
PGSPTADDETAGIULYGSSNIDSDVEDSTIRQWLNVHRQVINDVRRNLKAKGSETLAL
GQLACRILFATKAIGFDAGSQQTPFLLPNASRRYESRWLNFKIPEDTKAVAFRDLRGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MITRELQLLAYTAEPSALETAALARSIPGLQNVIIQTQDAYLVTFTTSPRPLREHQLKIETLLFIKAALRTFDEQQYLPIPLSALSSSFTFYYGPDINRL
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5'RACE-PCR"
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RRRIFEEQQEKGLINLKYENSRLRCQVEKRKDEIRILÆWLNYHKCTTLQNYNIGPPE
PRVKYENSLEMQCATAFINLDQQYTMNLNIPETVSGNTTNGFAAATAFIHTNCYEK
TLANNTNIFEAKLNCEVLPSFTSALDDLLSIDWNNLYNL"
                                                                                                     HYRSLLRTNLRHTFNFETQQLDFPHADRRGAVPHDNPQYIPMDAMDPSQ'
                                                                                                                                              VLPCWVQGTHLGFSHNNITFFGDLETRQQVAATFNGPLVQSGPAREYPLNPTEAEHPY
AGLCSEDGRHLALLFDPCLAFNTWQWQHNQTGPGQGELPVSPWKLMFYRLYNWSKFHQ
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/product="tegument protein"
/protein_id="AAC58056.1"
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LDSDSFQFPRRNSSCNCTREEATRTLLEALKRALQIIAGYINETDTEELPTYPPTMTT
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                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSRPIVTLPVVVNKYTGIAGNAQLFQSANLGYFMGRGVDKNLLGDSLFVKKQQNSYMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKYAEAGAFSLPLLHGVTVEEAFVPNVKAVYKKIDMTTVSVKLSTFYNRAIIFHNVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMEPQDWICSNFNEFYTIHETDLNGVQYECWKYLRELVLSVALYNITWEKNLCIYRTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SREYLSTLRLHFFALITGPLTTQEGLFPSPPNVQLAHCLEAAHFMPHQKMLLNEMIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQFVAFEEEQVKLTSMDHSGKVVGGKKRKIATMFDDLDL"
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                                                                                                                                                                                                 LTAAVVITVILLNRKAKRFAQNPVQMIYPDIKTITSQREELQVDPISKHELDRIMLAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-973-363-11 to: N_Geneseq_032802:*
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): 523.620000
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DT 12-MAR-1997 (first entry)
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XX
Bird; sex determination; chromodom
KW CHD-W; chromodomain-Helicase-DNA b
XX
Gallus sp.

XX
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CC (AAM08144) sequence are provided o
a proportion of chicken CHD-1a clo
CC between bases 4327 and 4328 of the CC
CAAM08149. None of the 7 CHD-1 c
CC complete motif. There are no spli
CC CANTALTSI). None of the 7 CHD-1 c
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alignment_block:
US-08-973-363-11 x AAT42752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA06801
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA06851
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS28888
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS28894
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA06800
                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                          A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                                                                                                                   Sequence 265 BP; 158 A; 16 C; 61 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn, and to control sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key Location/Qualifiers misc_difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "base 52 disrupts the reading frame for
the_translated amino acid sequence given
                                                                                              432.00
4.909
98.876
                                                                                                  Length: 89
Gaps: 1
Percent Identity: 98.876
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261
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from:

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seq_documentation_block:
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A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-1A clones (see also AAT42752).
                                                                                                                                                                                                                                                                         Griffiths R,
                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT42753;
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                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                      Avian
                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1996
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                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAla
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                                                                                                                                                                                                                                        1997-043127/04.
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                                                                                                                                                                     chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHD-W clone CC14 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 137
                                                                                                                                                                                                                                                                                                           INNOVATION LTD
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                                                                                                                                                                                                                                                                         Tiwari
                                                                                                                                                                                                                                                                                                                                            95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                            96WO-GB01341
                                                                                                                                     7; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "base 52 disrupts the reading frame
the translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromodomain-Helicase-DNA binding case-DNA binding on the W chromoson
                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
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seq_documentation_block:
ID AAS90688 standard;
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US-08-973-363-11 x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCM) primers, Oligomers, and for chromosome polymerase and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                  The
                                                                                                                                           diagnostics, for responsible for
                                                                                                                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
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                                                                                                         Claim
                                                                                                                                                                   New isolated
                                                                                                                                                                                                                                                                                                             30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                    11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluLysArgGluThrLysGluLysGluAsnLys 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGGATTGTTTCAGTGAAAACATCCACATAAAAAAATAAAAGCAGAAAA
                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGAAAAAAGAGAGAAAAGAGAAAGGAAAATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-639362/73.
DB; ABG26501.
                                                                                                                                                                                                                                                                                                                                                                                                        supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome mapping;
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                                                                                                                                                                                                                                                   HYSEQ
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                                                                                                         SEQ
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                                                                                                                                          polynucleotide and encoded polypeptides, useful forensics, gene mapping, identification of mutator genetic disorders or other traits and to asso
                                                                                                                                                                                                                             Liu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                         2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                             2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                            novel
                                                                                                                                                                                                                                                   INC.
                                                                                 relates to isolated
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                                                                                                                                                                                                                                                                                                                                                                                                       e mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder;
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4.390
89.130
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                                                                                                                                                                                                                                                                                                                                                                                                                                           human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cdna;
                                                                                                         26492;
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                                                                                                      103pp;
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                                                                                                       English.
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Identity:
                                                                                 polynucleotide (I) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
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                                                                                                                                            mutations
o assess
                        techniques
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3363636363636%&

Sequence 621 BP; 324 A;

36 C;

227 G;

34 T; 0 other;

quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.

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alignment_block:
US-08-973-363-11 x AAS90688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
Ratio:
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS46691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAS90688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
 15-MAR-2000;
06-APR-2000;
07-APR-2000;
                                                                                                                                           Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                         294
                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                              15-MAR-2001; 2001WO-EP02955
                                                                      20-SEP-2001.
                                                                                             WO200168912-A2
                                                                                                                   Homo sapiens.
                                                                                                                                                                                       Tumour suppressor gene derived chemically modified sequence #414.
                                                                                                                                                                                                                18-DEC-2001
                                                                                                                                                                                                                                                              AAS46691 standard; DNA; 24259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 GGAG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr
                                                                                                                                                                                                                                                                                                                                                                                                                                  sValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                       AspLysLysGluLeuLysGluLysAspAsnLysGluLysArgGluAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159.50
2.573
75.610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . AAGAAGGAGAAGGAGAAGGAGGAGAAGGAGA
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Gaps:
Percent Identity:
                                                                                                                                                                                                                                                               ВP
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1
41.463
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alignment_block:
US-08-973-363-11 x AAS46691/rev
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Cl is missing). Disside and ID 535, except for those whose partner sequence (c.g. as a signal).
                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AAS46691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                      11996
                                                                                                                                                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                  GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsnLy 67
sGluLysArgGluAsnLysValLysGluSerThrGlnLysGluLysGluV 84
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromos and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence that it is the sequence of the property of the
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23-AUG-2000;
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ID AAS90715 standard; cDNA; 693 BP.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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WO200175067-A2
                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #26519.
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 luLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LeuLys......GluLysAspAsnLysGluLysAr 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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75.294
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Gaps: 2
Percent Identity: 41.176
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alignment_block:
US-08-973-363-11 x AAS90715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polynucrase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC in restore normal activity of (II) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC are possible for genetic disorders or other traits to assess biodiversity CC amino acid sequences. AA664197-AA694564 represent novel human CC diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. and top. but by bublished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAS90715 from: 1 to: 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
387 GGAGGAGGAGAAGAAGAAGAAGGAGAAGGAGAAGGTGAAGGAGA 436
                                                                                    Sequence 693 BP; 296 A; 79 C; 234 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 26519; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG26528.
                  44 snLysArgGluLeuLysArgGluLysLysGluLysGluAspLysLysGlu 60 ::|||::::: ||||::: ||||:::
                                                                                                                                                                                                                                                                                                                                                                                                  11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27
                                                                                                                         61 LeuLys......GluLysAspAsnLysGluLysAr 70
                                                                                                                                                                                                                                                                                                           27 eGlyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
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Ratio:
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75.294
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Gaps: 2
Percent Identity: 41.176
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AGAAG 441

87

luLys

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seq_documentation_block:
ID ABL33958 standard; Db
XX
ABL33958;
XX
ABL33958;
XX
ABL33958;
XX
DT 26-MAR-2002 (first e
XX
Human immune system
KW Human; immune system
KW Human; immune system
KW antiarteriosclerotic;
KW neuroprotective; antial
ABL33958;
XX
Human immune system
KW antinflammatory; can
KW acute myeloid leukaen
KW antirheumatic; antial
ABC acute myeloid leukaen
KW antirheumatory; can
KW acute myeloid leukaen
KW neurofibromatosis; ri
KW gene; ds.
XX
OS Homo sapiens.
XX
YOS USENCE ON THE PROPERS AND THE AND THE MARK
XX
YOS OLAIM 1; SEQ ID NO 15
XX
YOS The present invention
CC Genes which are modifice
CC macular degeneration,
CC Including eye disease
CC macular degeneration
CC Including Alzheimer'
CC The present
CC diseases. The present
XX
SQ Sequence 14006 BP; 33
                                                                                                                          alignment_block:
US-08-973-363-11 x
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                                                                                 Align seg 1/1
                                                                                                                                                                                              Percent Similarity:
2299
                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                    LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr
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                                                                                                                                                                                                                                          Quality:
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                                                                               reverse of: ABL33958
                                                                                                                            ABL33958/rev
                                                                                                                                                                                          156.00
2.438
78.049
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Percent Identity:
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seq_name:
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The complex complex combinates are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques complex                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2099
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23-AUG-2000;
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DB; ABG26538.
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2000US-0649167.
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medical imaging; diagnostic; genetic disorder;
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SSSSSSS

diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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seq_documentation_block:
ID ABA58819 standard;
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US-08-973-363-11 x AAS90725
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAS90725
                                                                           04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0608408; 30-JUN-2000; 2000US-0608408; 03-MUG-2000; 2000US-0632366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0236359; 04-OCT-2000; 2000GB-0024263.
            WPI;
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                                 Penn
                                                       (MOLE-)
                                                                                                                                                                      30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                             09-AUG-2001.
                                                                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                                                                                                                                                    Human foetal liver single exon nucleic acid probe #7124.
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                                 SG,
                                                        MOLECULAR DYNAMICS INC.
                                 Hanzel DK,
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2.681
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Gaps: 2
Percent Identity: 44.444
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alignment_block:
US-08-973-363-11 x ABA58819/rev
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ID ABA27737 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:ABA27737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
                                                                                                                                                                                                                                     Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 7124; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                             30-JAN-2001; 2001WO-US00666
                                                                                                          09-AUG-2001
                                                                                                                                                   WO200157274-A2
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                    Probe #6203 for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 475 BP; 38 A; 198 C; 45 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AspLysCluLeuLysGluLys...AspAsnLysGluLysArgGluAs 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
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Ratio:
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Gaps: 2
Percent Identity: 42.169
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alignment_block:
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                             documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the prespecification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
 Human brain
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Similarity:
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2000US-0632366.
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probe
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alignment_scores:
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US-08-973-363-11 x AAK06973/rev
                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                            Percent Similarity:
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                    brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; microarray; Alzheimer's disea epilepsy; cancer; ss.
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30-JUN-2000;
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          nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys
                                         AspLysLysGluLeuLysGluLys...AspAsnLysGluLysArgGluAs 72
                                                                               ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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alignment_block:
US-08-973-363-11 x AAK32709/rev
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ID AAK32709 standard; DNA; 475 BP
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                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AAK32709 from: 1 to: 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, Leukaemia and myeloma. The present sequence is one of the probes of the invention.
                           Sequence 475 BP; 38 A; 198 C; 45 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone {\tt marrow} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK32709;
                                                                                                                    Example 4; SEQ ID NO: 7266; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157276-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                      40 ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
                                                                                                                                                               23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
                                                                                                                                                                                                                                                      7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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2.430
77.108
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Percent Identity: 42.169
                                                                                                                                                                                  alignment_block:
US-08-973-363-11 x AAT38524/rev
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                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
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                                                                                                                                                                                                                                                      Ratio: 2.430 Percent Similarity: 77.108
                                                                                                                                          Align seg 1/1 to reverse of: AAI38524 from: 1 to: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-EEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234587.

27-SEP-2000; 2000US-023559.

04-OCT-2000; 2000GB-0024263.
                                                364 AAACAGAAGAAGAAGGAAGAAGGAGGAGGAGGAGGAGGAAGGA 315
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 475 BP; 38 A; 198 C; 45 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 7210; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488897/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #7210 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI38524 standard; DNA; 475 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
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23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                           7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
                                                                                                                                                                                                                                                                            Quality:
Ratio:
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ID ABA71159 standard; DN
XX
AC ABA71159;
XX
DT 01-FEB-2002 (first e
XX
DT 01-FEB-2002 (first e
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DT 01-FEB-2002 (first e
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DE Human foetal liver;
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KW Human; foetal liver;
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KW Human; foetal liver;
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WO200157277-A2.
XX
PN WO200157277-A2.
XX
Q9-AUG-2001; 2001W0-1
XX
PN 04-FEB-2000; 2000US-1
PR 26-MAY-2000; 2000US-1
PR 30-JUN-2000; 2000US-1
PR 30-JUN-2000; 2000US-1
PR 30-JUN-2000; 2000US-1
PR 21-SEP-2000; 2000US-1

alignment_scores:
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                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 19464; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human foetal liver single exon nucleic acid probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0226359.
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155.50
2.430
77.108
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                        Length:
                                                                                                                                                                         235 T; 0 other;
83
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42.169
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alignment_block:
US-08-973-363-11 x ABA71159/rev
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                                                                                                                                                                               23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
79
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                                                                                                                         ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu
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                                                                              AspLysGluLeuLysGluLys...AspAsnLysGluLysArgGluAs 72
                                                                                                          reverse of: ABA71159
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31
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i AG040837 Pan troglodytes DNA i AG061359 Pan troglodytes DNA i BG533694 602562348F1 NIH_MGC i BG539033 602568396F1 NIH_MG i BM168323 EST570846 PyBS Plas

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gb_est1:RA742163
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gb_gss:RA230981
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gb_gss:RA231298
gb_gss:RA2312171
gb_gss:RA2312209
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Query: US-08-97:
Query length: 88
Database: EST:*
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Database length: -1841457050
Search time (sec): 4390.400000
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Copyright (c) 1993-2000 Compugen
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    | Documentation
| BMO1557 603
| AA74853 0a5
| AI74213 qh8
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| AI74213 qh8
| AI74213 qh7
| AI76995 140
| AI890775 wm9
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| AI890775 mm9
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97 603641828F1 NIH_MGC_87
63 0457609.51 NCI_CGAP_GC
63 0457609.51 NCI_CGAP_GC
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64 EST571461 PyBS Plasmod
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64 EST571461 PyBS Plasmod
64 EST571465 PyBS Plasmod
64 EST571625 PyBS Plasmod
64 EST570425 PyBS Plasmod
65 EST570425 PyBS Plasmod
66 EST570425 PyBS Plasmod
67 EST67253-34818.TJ RPCI
68 EST570425 PyBS Plasmod
69 EST570425 PyBS Plasmod
60 EST570425 PyBS Plasmod
61 MRILST0088-10119-003
61 MRILST0088-10119-003
62 Pan troglodytes DNA,
63 Pan troglodytes DNA,
64 Pan troglodytes DNA,
65 Pan troglodytes DNA,
66 EST57047 PyBB Homo sapi
67 EST5041.01_Sp6E RP
68 Pan troglodytes DNA,
69 Pan troglodytes DNA,
69 Pan troglodytes DNA,
69 Pan troglodytes DNA,
61 PRESCATTF Entamoeba hi
60 EST5041.01_Sp6E RP
60 EST5041.01_Sp6E RP
61 EST5041.01_Sp6E RP
61 EST5041.01_Sp6E RP
61 EST5041.01_Sp6E RP
61 EST5042.07_T7 CIT
61 EST5043.07_T7 CIT
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gb_gss:AG061359
gb_est2:BG533694
gb_est2:BG539033
gb_est2:BM168323
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US-08-973-363-11 x
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                                                                                                                                                                                   140 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG
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                                     17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG
                                                                                                                                                                                                                                                                                                                             90
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 677)

RS NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12066 row: g column: 08
High quality sequence stop: 674.

S Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAAACAGAAAG
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//db_xref="taxon:9066"
//db_xref="taxon:9066"
//clone=lib="NHI_MGC.87"
//clone_lib="NHI_MGC.87"
//lab_host-*DH10B (phage-resistant)"
//note="Organ: breast; Vector: pCWV-SPORT6; Site_1: Not1;
//note="Organ: breast; Vector: p
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Gaps: 1
Percent Identity: 77.528
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allma
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 343)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome

DNA Sequencing by: Washington Clone distribution

Clone distribution: NCI-CGAP Clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 343)
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                                                                                                             62
                                                                                                      Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

10 17 t
                                                                                                                                                                                                                                     /clone="IMAGE:1309072"
/clone_lib="NCI_CGAP_GCB1"
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/db_xref="taxon:9606"
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Length:
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US-08-973-363-11 x AA748563/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 luGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sGluLys 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGATAAAAGAAAAAGAGATAAGAAAGATATAAAGGAAAAAGATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGACAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAAAGAGGGAAGCAAAAGAAAAGGAGAATAAAAAAAGAACTTAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AT242163
430 bp mRNA linear EST 01-DEC-1991 gh81f02.xl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI242163.1 GI:3837560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI242163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 429
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen lNFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1851099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.317
91.304
                                                                                                                                                                                                                                    /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                          /dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Std Error: 0.00
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REFERENCE
AUTHORS
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VERSION
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Quality:
Ratio:
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US-08-973-363-11 x AI242163/rev
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GAGATAAAAGAAAAAGATAAGAAAGATATAAAGGAAAAAGATTTTAA 7
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 456)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
Mhite,Y., Wylie,T., Waterston,R. and Wilson,R.
MashU-NCI human EST project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA699918 456 bp mRNA linear EST 19-DEC-1997 z161612_s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone_IMAGE:435311 3', mRNA sequence.
                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Seq primer: -40mil frd. ET from Amersham
High quality sequence stop: 420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA699918.1 GI:2702881
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4.371
91.176
/db_xref="taxon:9606"
/clone="IMAGE:435311"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
                                                                                 /organism="Homo sapiens"
/db_xref="GDB:1335080"
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 68
Gaps: 0
Percent Identity: 77.941
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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US-08-973-363-11 x AA699918/rev
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ORIGIN
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LOCUS BF239967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 AAGAAAAGAGGAAAGGAAAAAGGAGAATAAAAAAAAACTTAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AGACAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAAACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 luGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysArg
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Mammalia; Eutheria; Primates; Catarihini; Hominidae; Homo.

E 1 (bases 1 to 821)

E 1 (bases 1 to 821)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                   601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5', BF239967
                                                                                                                                                                                                                                                                       BF239967.1 GI:11153890
EST.
                                                                                                                                                                                                                                        Homo sapiens
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4.361
91.045
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Gaps: 0
Percent Identity: 77.612
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BASE COUNT
ORIGIN
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                     REFERENCE
                                                                                SOURCE
                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                             seq_documentation_block:
LOCUS BM168938
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                                                                                                                             VERSION
                                                                                                                                                ACCESSION
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    AUTHORS
                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 AGACCAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 sGlu.AsnGluGluLysProGluProAspIleGlyIleLysLysGluAla 33
                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                        LysGluLysArgGluAsnLysValLysGluSerThrGlnLysGluLysGl 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAGATAAAAGAAAAAGAGGATAAGAAAGATAT . AAGGAACAAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g.GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsn 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysAr
                                                                                                                                                                                                                                                                                                                                                                                                   AAAGAAAAACGAGAAAACCAAAGTAAAAGAAGCTATACAGAACGAAAAAG
                                                                                                                                                                                                                                                                                                                     ACTAAAGGACGAAAAG 498
                            Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                   BM168938 660 bp mRNA linear EST 04-DEC-2001 EST571461 PyBS Plasmodium yoelii yoelii cDNA clone PYCPJ56 5' end,
                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LICM1033 row: k column: 18 High quality sequence stop: 562.
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
                                                                                                                           BM168938.1 GI:17302170
                                                                                                                                                BM168938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                     (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); Distranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266.00
3.367
87.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:4133129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_54"
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Gaps: 2
Percent Identity: 68.889
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JOURNAL
COMMENT
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ORIGIN
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Align seg 1/1 to: BM168938
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                                                                          54 AGAAGAAAAAAGGATGAAAAGGAAGAAAAGGAAGAAAAAGAAAAGAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspI1
                                                                                                                                                                                                                                                                                                                                                                                                4 CGCGAGTTGANAACTGAGANAGTGGAAGAAAAGGAAAAGGAAAAGGAAAA
rThrGlnLysGluLysGluValLysGluGluLys
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                                                                                                                                                                                   LeuLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSe
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Contact: Jane Carlton
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The Institute for Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. coli XL-1 Blue"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothicyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to Hybrilap arms directionally using EcoRI XhoI cleaved arms.
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Gaps: 0
Percent Identity: 48.718
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LOCUS BM161742
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12 LysIleLysThrGluLysGluAsnGluGluLysFroGluProAspIleG1 28
8 GAGTTGAAAACTGAGAAAAGTGGAAAAAGGAAAAGGAAAAAGA 57
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Ratio:
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Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 605)
Carlton,J.M., Dalty.T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.W. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Dermater Carlton
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Fax: 301-838-0208
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
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EST564265 PyBS Plasmodium yoelii yoelii cDNA clone PYCKI49 5' end,
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primer: ADF.
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3.063
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37 c
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/clone="PYCKI49"
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/strain="17xL"
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Gaps: 0
Percent Identity: 49.351
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Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
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Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 640)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B
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EST570235 PyBS Plasmodium yoelii yoelii cDNA clone PYCOP51 5' end, mRNA sequence.
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For clone info, please contact the Malaria Research
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
                        358
                                                          /dev_stage "Assural blood stages"
//lab_host="E. coli XL-I Blue"
//lab_host="E. coli XL-I Blue"
//lab_host="E. pah-GALA, At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanddinium isothiocyanate method, and mRNA isolated using the guanddinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl 5-500 column.
Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAb-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
                     isolated."
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.M. and Carucci,D.J.
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/clone="pycOp51"
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/strain="17XL"
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US-08-973-363-11 x BM167712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LysIleLysThrGluLysGluAsnGluGluLysProGluProAspIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSerTh 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluAsnL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ysArgGluLeuLysArgGluLysLysGluLysGluAspLysLysGluLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAGAGAAAAAGAAAGGAAAGAAAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                    Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (Pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 348 row: I column: 8

Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Other_GSSs: RPCI-23-34818.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPCI-23-34818.TJ RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K.,
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ009894
                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A2009894.1 GI:7085278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                louse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinretins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-34818"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193.00
3.063
81.818
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Gaps: 0
Identity: 49.351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                        MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A linear GSS 25-FEB-2000 genomic clone RPCI-23-34818,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Jong, P
                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est1:AL628267
                FEATURES
                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                 AUTHORS
TITLE
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                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456
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source
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alignment_block:
US-08-973-363-11 x AZ009894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LeuLysGlu...LysAspAsnLysGluLysArgGluAsnLysValLysGl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uSerThrGlnLysGluLysGluValLysGluGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eGlyTleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGACGAAGGAAGAAGGAGGAGAAGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AAGAAGGAGAAGAAGGAGAAGAAGGAGAAGAAGGAGAAGAAGG
                                                                                             Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas009e08.sp6
                                                                                                                                                                                                            xenopodinae; Silurana.
1 (bases 1 to 507)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                 Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL628267 XGC-gastrula Silurana tropicalis
                           constructed by Aaron M. Zorn.
                                              Sequencing primer: SP6
This sequence is from a Xenopus
                                                                                                                                                                                             Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                western clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL628267.1 GI:16597750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                  Hinxton, Cambridgeshire, CB10 1SA,
                                                                                                                                                                                                                                                                                                                                                             Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 121\ c 167\ g 104\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: Kidney/Brain: Vector: pBACe3.6; Site_1:
ECORI: Site_2: ECORI: Female C57BL/6J mouse kidney and,
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190.50
2.977
81.013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
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Gaps:
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                                                 Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 02-NOV-2001
|e TGas009e08 5',
                                                                                                                                                                                                                                                                                                                                                             Pipidae;
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BASE COUNT

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alignment_block:
US-08-973-363-11 x AL628267
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LOCUS AI890775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est1:AI890775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AL628267 from: 1 to: 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 AAAAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 AAGAAAAGAAAGAGATA.....AAAGAAAATAAAAAGGACCCTAAGAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 AGAAAATGAGGACCGAACAGAGTTAGATGTCAGTGTTAACAAAGAGCCAG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 GAGGAAACTGTACCCCTCAGAACAAATAATAAAAGG...AGAGCAGAGAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 luGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysArg 50 |||||||||:::: |||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 alLys 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wm95f11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3'
similar to SW:CHD1_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING
PROTEIN 1; mRNA sequence.
A1890775.
A1890775.1 GI:5595939
                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 547)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                     Homo sapiens
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189.50
2.828
78.824
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/clone_lib="XGC-gastrula"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Bscherichia col1 XL1-blue"
/lab_host="Bscherichia col1 XL1-blue"
/note="Yector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Silurana tropicalis"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 44.706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                     COMMENT
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                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                              AUTHORS
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REFERENCE AUTHORS TITLE

ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

DEFINITION

COMMENT

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alignment_block:
US-08-973-363-11 x AI890775/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AZ008814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_gss:AZ008814
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Ratio: 4.375 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 77.273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AI890775 from: 1 to: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 luGluLysArgGluThrLysGluLysGluAsn 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                        Mouse BAC End Sequences from Library RPCI-23 (Inpublished (1999) (Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www.bio.llni.gov/bbrp/image/image.thml
Insert Length: 1924 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
Location/Qualifiers
                                    9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 634)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret, Devins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ008814 634 bp DNA linear GSS 25-FEB-2000 RPCI-23-38903.TJ RPCI-23 Mus musculus genomic clone RPCI-23-38903,
                                                                                                                                                                                                                                                                                     and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ008814.1 GI:7084198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence.
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szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2443725"
/clone=lib="NCI_GGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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VERSION
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US-08-973-363-11 x AZ008814
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SOURCE
                                                                                                   DEFINITION
                                                                                                                           seq_documentation_block: LOCUS AZ330985
                                                                                                                                                                                     seq_name:
                                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LysHisLeuHis......LysLysIleLysThrGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                              ArgGluLeuLysArgGluLysGluLysGluAspLysGluLeuLy 62
                                                                                                                                                                                                                                                                                                                   lnLysGluLys.....GluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                           sGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSerThrG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....AlaGluGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                             AGGAGGAGAAGGAGGAGGAGGAGGAGGAG
                                                                                                                                                                                   gb_gss:AZ330985
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Ratio:
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                                                                      AZ330985 743 bp DNA linear GSS 29-SEP-20
LM0056C22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0056C22 R, DNA sequence.
                 GSS
                                     AZ330985.1 GI:10393428
                                                           AZ330985
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house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " a 73 c 219 g 63 t 1 others
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2.703
67.368
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-38903"
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Gaps: 4
Percent Identity: 47.368
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to:
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869
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                                                                                                                                     11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27
                                         eGlyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
                                                                                         Mus musculus
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
1 (bases 1 to 743)
                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0056 row: C column: 22
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                           Ratio:
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  107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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80.769
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/db_xref="taxon:10090"
/clone="UUGC1M0056C22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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Rodentia;
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Gaps:
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LOCUS AZ952930
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Welss,R.
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2M0217N19R House 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0217N19 R, DNA sequence.
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Insert Length: 10000 Std Error: (
Plate: 0217 row: N column: 19
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 571.
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/5J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with 74 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114 (gb)AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0217N19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (2000)
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COMMENT

FEATURES

ACCESSION VERSION

KEYWORDS

REFERENCE

AUTHORS

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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US-08-973-363-11 x AZ952930
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Ratio: 2.664
Percent Similarity: 78.049
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 GAAGAAGAAGAAGAACAAGAAGAACAAGAACAAGAACAAGAA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 GAGAAGAAGGAGAAGAAGGAGGAGAAGGAGAACAAGAAGGAGAACAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AGAAGAAGAAGGAGAAGAAGGAGAAGAAGGAAGAAGGAAGAAGGAAGAAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 sValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AspLysLysGluLeuLysGluLysAspAsnLysGluLysArgGluAsnLy 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                      Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozker-Kalogeropoulos, O., Potter, S.,
Saurin, W., Pekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS, Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lepingle, A., Casaregola, S., Neuveglise, C., Bon, E., Nguyen, H., Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemlascomycetous yeasts: 14. Debaryomyces hansenii var. hansenii FEBS Lett. 487 (1), 82-86 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces. 1 (bases 1 to 981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Debaryomyces hansenii.
Debaryomyces hansenii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Debaryomyces hansenii, genomic survey sequence. AL437527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS07B7L 981 bp DNA linear GSS 08-JUL-2001 T3 end of clone BC0AA009H03 of library BC0AA from strain CBS 767 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL437527.1 GI:12220940
                                                                                                             Genoscope
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46 c 194 g 48 t
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                       887
                                                                                                                                                                            840 AAGARAGAT...AAGAACGAGAAGAAAGAAGAAAGATAAGAACGAGAA 886
                                                                                                                                                                                                                                                                    source
931 AGAAAGAAGAAGAAGAAGAAAGAAA 962
                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 AGTAAGCAGCATAAGAAGAAAAAAAATAAAGAAGGACCGTAAGAAAAAAGA 760
                                     78 hrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                 61 uLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSerT 78
                                                                                                                                                                                                                              45
                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                         LysArgGluLeuLysArgGluLysLysGluLysGluAspLysLysGluLe 61
                                                                                                                                                                                                                                                                                                lyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluAsn 44
                                                                                         GAAAGAGAAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4959"
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1 putative frameshift(s)"
/evidence=not_experimental
98 c 241 g 209 t 3
                                                                                       .....AAAGATAAGAACGAGGAGAAAGAAGAAAGAAGA 930
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68.085
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Search information block:
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Query : By-08-973-583-14
Query length: 45
Database: GenEmbl:*
Database: length: 1873333701
Search time (sec): 4907.710000
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9b_htg:AC021449
9b_htg:AC021449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_ov : AF004397
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-MODEL-frame+_P2n.mode1 -DEV-x1h
-Q-/cgn2_1/USPTO_spool/US08973363/runat_01082002_080050_18581/app_query.fasta_1.638
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137 ! A58694 Seque
6872 ! AF004397 Ga
37 | ASB664 Sequence 13 from Patent
B72 | ASB693 Sequence 12 from Patent
C1220 | AC002372 Homo sapiens chromo-
C1320 | AC002372 Homo sapiens chromo-
C1320 | AC002372 Homo sapiens chromo-
C1320 | AC002137 Homo sapiens chromo-
C1320 | AC002131 Homo sapiens chromo-
C1320 | AC002131 Homo sapiens chromo-
C1320 | AC002131 Homo sapiens chromo-
C1321 | AC002382 Homo sapiens chromo-
C1322 | AC008600 Rattus norvegicus chromo-
C1322 | AC008600 Rattus norvegicus chromo-
C1322 | AC003382 Homo sapiens genomi-
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C1322 | AC003385 Homo sapiens genomi-
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gb_htg:AC079533
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   Archosauria; Aves; Neognathae; Gall
Phasianinae; Gallus.
1 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
A CHB1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
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Sequence 13 from Patent WO9639505.
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/db_xref="taxon:32644"
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101 GGAGAAAAAGAGAGAGAAAGGAAAAGAAATAAG 136
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                                                                                                                                                                                                                                                                                                         AF004397 MRNA linear VRT 08-0C Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, compl
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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Gaps: 1
Percent Identity: 97.826
                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae;
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2013978 : AC079533 Mus musculus clo
49221 : AL450106 Human DNA sequenc
132755 : AC092536 Homo sapiens BAC
147541 : AC097032 Rattus norvegicu
chicken Gallus
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                         1 AspGlyIleValSerValLySHisProHisLySLySIleLySAlaGluLy 17
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 800, UK
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CKVLKQRPREYALKKOPSYIGGHESLELRDYOLNGLWALAHSWCKGNGCILADEWGLG
CKVLKQRPREYALKKOPSYIGGHESLELRDYOLNGLWALASWCKGNGCILADEWGLG
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MIRTHEWMHPQTKRLKRWILLTYYELLKDKSFLGGLWAAFIGVDEAHRLKNDDSILY
RTLLDPKSNHRLLITGTPLQNSLKELMSILHFIMPEKFSSWEDDEEEHGKGREYCYAS
LHKELEPFLLRRVKNDYEKSLPAKVEQILRMEMSALOKOYYKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQEALQHLIRSGKLILLDKLLIRLR
ERGNRYLIFSOMVRMLDILABYLKYROPPFQRLDGSKGELRKQALDHFNAEGSEDFC
FLLSTRAGGLGINLAASADTVYLFDSDWRPQNDLQAARAHRIGQKKQVNIYRLYTKGS
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LFKEPEGGEOEPGMDIDEILKRAETRENEFGPLTVODELLSQOKYANFSNMDEDDIE
LEPERNRRRWEELIPESGRRRIEEEERGKELEBIYNLFRMRNCAKOISFNGSEGRRSR
SRYYGGSDSDSTTERKRPKKRGRPTIFRENIFGPLTVODELLSQOKYANFSNMDEDDIE
LEPERNRRRWEELIPESGRRRIEEEERGKELEBIYNLFRMRNCAKOISFNGSEGRRSR
SRRYSGSDSDSTTERKRPKKRGRPTIFRENIKGFSDAEIRFETKSYKKGGPLEELD
AVARDAELVUKSETDLARLGELVHNGCIKALKONSSGOERAGGRLGKVRGPTFRISGV
QVNAKUTSHEEELAPLHKSIFSDPEEKKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
YEYGYGSWEMIKMDPDLSLTQKILPDDDKKPOAKQLQTRADYLLKLLNKDLARKEAQ
RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQSEKSKSDEDDEEEDNKDETYSVK
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SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWOMDHRASGSGPRSPLDQRSPYGSRSPLG
HRSPEEHSSDHKSTPEHTWSSRKT"
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KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
THVIRNPDVEKLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
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/gene="CHD-Z"
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LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
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NEEKRENKVKESTQKEKEVKEEKVNEMKSENKEKSKKIPLLDTPVHITATSEPVPISE
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/note="CHD protein with hydrophilic domain"
/codon_start=1
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/db_xref="GI:2501846"
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                  GAAGAAAAAAGAGAGACAAAAGAGAAGGAAAATAAA 136
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Sequence 12 from Patent W09639505.
A58693
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                             1 (bases 1 to 101220) DOE Joint Genome Institute and Stanford Human Genome Center.
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 101220)
                                                                                                                        AC092372
AC092372.3 GI:17402768
HTG.
                                                                                                                                                                    Homo sapiens chromosome 5 clone RP11-58M12, complete sequence
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Unpublished
                Direct Submission
                                                                                          Homo sapiens
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1. .265
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US-08-973-363-14 x AC092372/rev
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ACCESSION
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LOCUS AC012624
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

MOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AcC012624.
The number of bases overlapped is 90404.

Location/Qualifiers
Direct Submission
Direct Submission
Submitted (31-0CT-1999) Production Sequencing Facility, DOE Joint Submitted (31-0CT-1999) Production Sequencing Facility, DOE Joint Submitted (31-0CT-1999) Production Sequencing Facility, DOE Joint Submission (31-0CT-1999) Production Facility (31-0CT-1999) Production (31-0CT-1999) Producti
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Homo sapiens chromosome 5 clone CTD-2082117, compl
AC012624
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (03-7UL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                            2 (bases 1 to 134365)
DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
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/chromosome="5"
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LOCUS AC021444
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Align seg 1/1 to: AC012624 from: 1 to: 134365
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearrino, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FittHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McSwan, P., McGurk, A., McKernan, K., McChelman, R., McGurk, A., McKernan, K., McChelman, R., McCons, R., Meldim, J., Meneus, L., Morcwa, J., Naylor, J., McConnor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Narden, K.,
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On Jul 21, 2001 this sequence version replaced g1:14277267.
Location/Qualifiers
1. .134365
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Homo sapiens clone RP11-58M12, V
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Unpublished
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DOE Joint Genome Institute and Stanford Human Genome Center.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 143079)
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40414 a 24497 c 25503 g 43951 t
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Percent Identity: 68.889
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Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,

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FEATURES
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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Submitted (18-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced gi:7407963.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51831 51930: gap of 100 bp 51931 62619: contig of 10689 bp in lei 62620 62719: gap of 100 bp 62720 75408: contig of 12689 bp in lei 75409 75508: gap of 100 bp 75509 92516: contig of 17008 bp in lei 92517 92616: gap of 100 bp 92517 92616: gap of 100 bp 92517 106409: contig of 13793 bp in lei 92617 106409: contig of 13793 lei 92617 106409: contig of 13793 lei 92617 106409: contig of 13793 lei 92617 106409
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40512 43279: contig of 2768 bp
43280 43379: gap of 100 bp
43380 45979: gap of 3526 bp
43380 4705: gap of 100 bp
47006 51830: contig of 4825 bp
51831 51930: gap of 100 bp
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Center clone name: 58_M_12
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Contact: sequence_submissions@genome.wi.mit.edu
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106510 143079: conti
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38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
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38921. .40411
                                                         40512.
                                                                                                                                                                                                                                         clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="assembly_fragment"
                                                                                          /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC'
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BASE COUNT
ORIGIN
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SOURCE
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US-08-973-363-14 x AC021449
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                                                                                                                                                                      TITLE
                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                      AUTHORS
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                                                                -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                               Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mirchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                                                2 (bases 1 to 145659)
DOE Joint Genome Institute
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Homo sapiens chromosome 5 clone
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Center Project Name:
               Project Information
                                                Web site:
                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                    Sequencing of Human Chromosome
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. 26246 c 26678 g
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51931. .62619
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4.077
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/note="assembly_fragment
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                                              http://www.jgi.doe.gov
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Gaps: 0
Percent Identity: 68.889
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Center clone name: CIT-HSPC_480B11

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alignment_block:
US-08-973-363-14 x AC008531
                                                                                                                                                                                     seq_documentation_block:
LOCUS AC091946
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Quality:
                                                                                                                                                                                                                                                                                seq_name: gb_htg:AC091946
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Ratio: 4.077
Percent Similarity: 86.667
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Consensus quality: 142556 bases at least Q20
Consensus quality: 14374 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation.
*NOTE: This is a 'working draft' sequence. It currently
*consists of 7 contigs daps between the contigs
*are represented as runs of N. The order of the pieces
*is believed to be correct as given, however the sizes
*of the gaps between them are based on estimates that have
*provided by the submittor.
*This sequence will be replaced
*by the finished sequence as soon as it is available and
*the accession number will be preserved.
*56175 56274; gap of unknown length
*100975 110127; contig of 44600 bp in length
*100975 110974; gap of unknown length
*11328 118190; contig of 1404 bp in length
*11328 118291 119694; contig of 1404 bp in length
*113291 119694; contig of 1404 bp in length
*113298 123397; gap of unknown length
*113298 123397; contig of 5303 bp in length
*12398 123597; contig of 5303 bp in length
193446 bp DNA linear HTG 09-JUN-2001 Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
AC091946 AC091946.1 GI:14333882
HTG; HTGS_PHASE1.
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/db_xref="taxon:9606"
/chromesome="5"
/chone="5"-(alTech human BAC library C"
/chone=11b="C3T880 g 48609 t 600 other:
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Percent Identity: 68.889
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AUTHORS
TITLE
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ORGANISM
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Consensus quality: 180259 bases at least Q20
Consensus quality: 180757 bases at least Q20
Consensus quality: 180757 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
** NOTE: This is a 'working draft' sequence. It currently
** consists of 33 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
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Center Project Name: 544799
Center clone name: RPCI-11_36012
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Center: Joint Genome Institute
Center Code: JGI
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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8: gap of unknown length
7: contig of 1209 bp in length
3: contig of 1056 bp in length
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10: contig of 200 bp in length
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16: contig of 1487 bp in length
17: contig of unknown length
18: contig of unknown length
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i contig of 2366 bp in length
i gap of unknown length
contig of 2981 bp in length
gap of unknown length
contig of 3948 bp in length
definition of 3948 bp in length
contig of 3324 bp in length
           gap of unknown I contig of 4813 kgap of unknown I contig of 4585 l
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               8 bp in length
n length
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5 bp in length
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FEATURES

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/chromosome="5"
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Location/Qualifiers
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130883: contig of 6745 bp in length
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141544: contig of 10861 bp in length
141644: gap of unknown length
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LOCUS AC022121
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US-08-973-363-14 x AC026778/rev
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                        Homo sapiens chromosome AC022121
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WI-13675 G23101
SHGC-58345 G38487
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On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 195433)
                                                                                                                      HTG
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Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.
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/db_xref="taxon:9606"
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                                                                                                                                                                 seq_documentation_block:
LOCUS AC092382
                                                                                                                                                                                                                         seq_name: gb_htg:AC092382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AC022121 from: 1 to: 219258
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                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                      87874 AGACAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 87825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                           34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                            17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG 34 :::::::|||||||||
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Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-JAN-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 21928)
DOB Joint Genome Institute and Stanford Human Genome Center.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Homo sapiens
                                                                                                                276181 bp DNA linear HTG 03-JUL-200 Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE, 47 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHGC-103595 G57841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WI-13675 G23101
SHGC-58345 G38487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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DOE Joint Genome Institute.
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                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                              AC092382.1 GI:14589571
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4.077 Gaps: 0
86.667 Percent Identity: 68.889
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/ 42062 c 40933 g 64309 t
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1. .219258
                                                                                                                                                                 HTG 03-JUL-2001
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Consensus quality: 229677 bases at least Q40
Consensus quality: 256163 bases at least Q20
Consensus quality: 250163 bases at least Q20
Consensus quality: 25099 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Quality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary (ags) between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission Direct Submitted (03-UH-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center Project Name: 435334
Center clone name: RPCI-11_75H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalla: Butherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 276181)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
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DOE Joint Genome Institute.
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1161: gap of unknown length
2827: contig of 1666 bp in length
2927: gap of unknown length
4227: contig of 1300 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f unknown
g of 1327
f unknown
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       f unknown
y of 1399
f unknown
                                                                                            f unknown
g of 1785
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alignment_block:
US-08-973-363-14 x AC092382/rev
                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                           alignment_scores:
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                                                                     Quality:
Ratio:
Percent Similarity:
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146714
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86.667
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157994: contig of 11081 bp in 16
157994: gap of unknown length
171752: contig of 13758 bp in 16
171852: gap of unknown length
201687: contig of 29835 bp in 16
201787: gap of unknown length
231268: contig of 29481 bp in 16
231368: gap of unknown length
231368: gap of 44813 bp in 16
231368: contig of 44813 bp in 16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on Jul 14, 2000 this sequence version replaced gi:8919096. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA sequence from clone RP5-1185H19 on chromosome Contains part of a gene for a novel protein, STSs, GSSs island, complete sequence.

ALIZ1982
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                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chrl
RP5-1185H19 is from the library RPCI-5 constructed at Park Cancer Institute by the group of Pieter de Jong.
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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                                                                                                                                                                                                                                                                               sequence is the entire insert of clone RP5-1185H19 The true t end of clone RP5-1039L11 is at 65940 in this sequence.
/clone_lib="RPCI-5"
26. .677
/note="L1M4 repeat:
                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                                   /map="p13.1-13.3"
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/note=". _region 15885.	/note="I region 15675.	<pre>/note="LlPB2 repeat: matches 57286 repeat_region 1543015473</pre>	15355	.14566	.14206 L2 repeat: matches 26982750	repeat: matches 1301	/note="	"Alusx repeat: matches 1300		/note="	/note="	/note=" 11102.	/note="	/note="L2 repeat: matches 15011795 1068310798	<pre>/note="Alusx repeat: matches 12297 repeat_region 983010110</pre>	<pre>/note="L2 repeat: matches 1/942359 of repeat_region 94939774</pre>	A/ repeat: matches 58/3.	er ta 95% conse	2 mer tt /3%	7408	.7353	2366	repeat: ma	ies 2	6579 ° match: STS: Em:HSPE07G05"	<pre>repeat_region 59516306 /note="L2 repeat: matches 23502730</pre>		390	misc_feature 51535836 Em.: AO629810"	match: GSS: Em:A0045996"	match: STS: Em:G5		matches 1296 o	21192626 /note="L1M4 repeat: matches -11498	repeat: matches 1853.	repeat_region 9681628 /note="L1M4 repeat: matches 17702452	/note="AluSx repeat: matches 1293
of consensus" repeat_region	of consensus" repeat_region	.6155 of consensus" repeat_region	consensus"		Consensus"	of consensus" misc_feature	repeat_region	of consensus" misc_feature	48 of consensus" misc_feature	of consensus" misc_feature	misc_feature	of consensus" repeat_region	7 of consensus" repeat_region	of consensus" misc_feature	of consensus" repeat_region	of consensus" misc_feature	of consensus" repea	misc_fe	repea			Of CONSONSIIS.	consensus"			of consensus"		of Consensus"	reneat region	reneat region	107000 + 1070000000000000000000000000000		of consensus	of consensus" repeat	of consensus" repeat	of consensus"	of consensus" repeat_region
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                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (05-APR-2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave Bronx, NY 10461, USA
On Apr 5, 2001 this sequence version replaced gi:13194207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-APR-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
3 (bases 1 to 219769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Han, J., Montgomery, K.T., Grills, G., Lee, E., Lon Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Gordon, M., Goltz, J.S. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC067964 219769 bp DNA linear ROD 05-APR-Mus Musculus Strain C57BL6/J Chromosome 5 RP23-337K7, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550).
                                                                                                                        CLONE LENGIH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon, M., Goltz, J.S. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Han,J., Montgomery,K.T., Grills,G., Lee,E., Lor
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R., Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A., Gordon,M., Goltz,J.S. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Mouse Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC067964.18 GI:13549252
                                                                                                         overlaps
                                                                                                                                                                                                 Contact: gnktm@capecod.bwh.harvard.edu
                                                                                                                                                                                                                                              http://wchanning.bwh.harvard.edu:9088/hpcgg/jsp/hpcgg/Sequence/mous
                                                                                                                                                                                                                                                                                                                       Harvard Partners Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 219769)
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                                                                                                         are noted
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3.138
76.316
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Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                Center:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 104780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Long, J., Pomerantz, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perera, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perera, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROD 05-APR-2001
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and CDNA sequences in Unique. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation as Low Coverage. Low coverage linkages are verified by PCR product size verification or verification of forward and reverse reads from clones which span the low coverage area.

bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality. QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000

Assembly program: Phrap version 0.990319 Contid length: 219769 Fraction of Phrap value < 40: 0.00293 Error Rate in Consed: 0.07 per 10,000 bases Number of N's in consensus: 0 Center project name: ACS Sequencing vector: pUC18; L08752 Chemistry: Dye-terminator Big Dye; 100% Summary Statistics

Distribution of Quality < 40 Bases:

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bases
                   1000
900
800
700
600
500
400
    σ,
    10
Phrap
    15
Value
Range
    35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7600...8061)
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complement(7603...7618)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="(TTTTC)n"
complement(1828. .1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="AT_rich"
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.11629
                                                                                                                                                                                                                                                                                                                                                                                                                 ly="(CA)n"
                                                                                                                                                                  y-"RMER17C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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US-08-973-363-14 x AC067964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AL589701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ro:AL589701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202076 GAGAAGAAGAAGGAAAGGAAAGGAAAGGAAAG 202110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
AL Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:17384104. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at hitp://www.chori.org/bacpac/home.htm vECTOR: pBACe3.6 the entire insert of clone RP23-202F3 The true left end of clone RP23-171015 is at 179556 in this sequence. The true right end of clone RP23-153B6 is at 117857 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus

1. (bases 1 to 219200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALD89701 219200 bp DNA linear ROD 30-JAN-2002 Mouse DNA sequence from clone RP23-202F3 on chromosome 13. AL589701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phillimore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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2.734
71.111
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Gaps: 1
Percent Identity: 44.444
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REFERENCE
AUTHORS
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US-08-973-363-14 x AL589701/rev
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ORIGIN
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LOCUS AC098600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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           E 1 (bases 1 to 231947)

E 1 (bases 1 to 231947)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Are, J.R., Banks, T., Barbaria, J., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garzan, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Holloway, C., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, F., Jackson, F., Jackson, F., Johnson, R., Jolivet, S., J., Jackson, F., Jackson, F., Johnson, R., Johnson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, 62 unordered pieces AC098600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACO98600 231947 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus chromosome Rfl clone CH230-95C8, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1;
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   Jackson,L.E., Jacobson,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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/note="Single clone region. Sequence from reads from a short insert library derived from a clone PCR. Restriction digest data confirm the assembly." a 46953 c 46966 g 61646 t
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3.346
74.286
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3942. .4127
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/chromosome="13"
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Jia,Y.,
   Johnson, R., Jolivet, S
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0
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64519:

gap of contig gap of

f unknown g of 6677 unknown

length bp in length length 56516:

2: gap of unknown length
5: contig of 10284 bp in length
6: gap of unknown length
7: contig of 6720 bp in length
7: contig of 6720 bp in length
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7: contig of 7803 bp in length

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Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, R., Tangy, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Mei, G., Morris, S., Moser, M., Neal, D., Newtson, J., Newt
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Direct Submission
Submitted (26-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

**NOTE: This is a 'working draft' sequence. It currently
consists of 62 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 191710 bases at least Q40 consensus quality: 199153 bases at least Q30 consensus quality: 203798 bases at least Q30 Estimated insert size: 197288; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 3.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GIKD Center clone name: CH230-95C8 Center clone name: CH230-95C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
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11491
11591
21784
21884
30103
30203
40487
40587
47307
47307
56617
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21883:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11590:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 11490 bp in length gap of unknown length contig of 10193 bp in length
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REFERENCE AUTHORS

JOURNAL TITLE TITLE

JOURNAL

COMMENT

in length y bp in length n length n length li bp in length n length length length length length length n length		bp in length
21458 ATGANGAANGANGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	* 218235 21834; gap of unknown length * 218335 219342; contig of 1008 bp in length * 219343 219442; gap of unknown length * 219443 220550; contig of 1108 bp in length * 219551 220550; contig of 1108 bp in length * 220551 220550; contig of 1561 bp in length * 220212 22211; contig of 1561 bp in length * 222212 22211; contig of 1781 bp in length * 222312 224092; contig of 1781 bp in length * 222312 224092; contig of 1781 bp in length * 224093 224192; gap of unknown length * 224093 224192; gap of unknown length * 254093 224	* 206063 206162: gap of unknown length * 206163 207721: contig of 1559 bp in length * 207722 207821: gap of unknown length * 207722 20574: contig of 2753 bp in length * 207825 210574: gap of unknown length * 210575 212188: contig of 1514 bp in length * 212189 212288: gap of unknown length * 212189 213701: contig of 1413 bp in length * 212180 213701: contig of 1746 bp in length * 213702 213801: gap of unknown length * 21548 215547: contig of 1746 bp in length * 21548 215547: gap of unknown length * 215548 215547: gap of unknown length * 217054 217153: gap of unknown length * 217054 217153: gap of unknown length

409

gap of contig ga

of 630 of 630 of 630 of 630 of 630 of 630 of 5957 of 4000 of 3985 of 4000 of 3985 of 4000 of 3985 of 4000 of 3985 of 4000 of 4000 of 4100 of 4100 of 4000

190895 193028 193128 195041 195041 195141 196416 196416 198846 198846 198946 201855 201855 201855 203550 203550 181701: 181801: 183811: 183911: 183953: 185953: 186053:

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Search information block:
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Query: Ength: 45
Query length: 45
Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 85845721
Search time (sec): 523.620000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: Aug 3, 2002 4:34 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MODEL-frame+_p2n.model -DEV=x1h
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-USCR-US08973363 -QGOL1_186 -NCPU=6 -ICPU=3 -LONGLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of: US-08-973-363-14 to: N_Geneseq_032802:*
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188 46 0.0377

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187 20 0.1394

178 26 0.1394

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178 26 0.1394
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alignment_block:
US-08-973-363-14 x AAT42753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL21448 - 
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Ratio: 4.889
Percent Similarity: 97.826
                                                          Align seg 1/1 to: AAT42753
                                                                                                                                                                                                                                             A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CBD-W clone CCl4 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-la clones (see also AAT42752).
                                                                                                                                                                                                                     Sequence 137 BP; 75 A; 10 C; 34 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers misc_difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD^-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken CHD-W clone CC14 3' motif.
/*tag= a
/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
in Fig 7"
                                                          from:
                                                                                                                             Length: 46
Gaps: 1
Percent Identity: 97.826
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163.24
161.47
172.30
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.95
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us-08-973-363-14
                                                   alignment_scores:
Quality:
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                               Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
AAT42752 standard;
                                                                                                                            A composite nucleotide sequence (AAT42752) and putative translate (AAW08144) sequence are provided of a motif that is found splice a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites with the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of
                                                                                                                    product of splicing.
CHD-W clone CC14 (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bird;
                                                                                                                                                                                                                             Disclosure; Fig
                                                                                                                                                                                                                                                              Avian
                                                                                                                                                                                                                                                                                              WPI; 1997-043127/04
                                                                                                                                                                                                                                                                                                                  Griffiths R,
                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken CHD-1A insert motif.
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                                                                                               Sequence 265
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                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS
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                              Ratio:
Similarity:
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                                                                                                                                                                                                                                                chromodomain-helicase-DNA binding genes determine sex — used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex determination; chromodomain-Helicase-DNA binding 1 chromodomain-Helicase-DNA binding on the W chromosome;
                                                                                                                                                                                                                                                                                   AAW08144.
×
                                                                                               ВP;
                                                                                                                                                                                                                                                                                                                                        INNOVATION
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                                                                                                                                                                                                                                                                                                                   Tiwari
AAT42752
                                                                                                                                                                                                                                                                                                                                                            95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB01341
                                                                                                                                                                                                                             7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 52
                             180.00
4.390
89.130
                                                                                               158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*taq=
                                                                                                                    (see also AAT42753).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA;
                                                                                              A; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                            "base 52 disrupts the reading frame the translated amino acid sequence in Fig 7"
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                            Identity:
                                         Length:
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84.783
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alignment_block: US-08-973-363-14 \times 
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ID AAA64139 standard:
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                                       Percent Similarity:
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                                                                                                                                          an antigen of the membranous structure of the inner ear protein, and is reactive with antibodies from patients having Meniere's disease. Meniere's disease is a chronic ear disease with unknown etiology. Serum from patients suffering from this disease contain autoantibodies against a 30 kDa cochlear protein antigen. The disease is believed to i an autoimmune disease. The beta-tubulin antigen is useful as a target substance in diagnosing or detecting Meniere's disease and in distinguishing this disease from other autoimmune ear diseases.
                                                                                                                     Sequence
                                                                                                                                                                                                                                                       The present
                                                                                                                                                                                                                                                                                   Claim 3;
                                                                                                                                                                                                                                                                                                            autoimmune ear diseases
                                                                                                                                                                                                                                                                                                                      New beta-tubulin antigen in the membranous structure of the inner reactive with antibodies of patients with Meniere's disease, for diagnosing Meniere's disease and distinguishing this disease from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic ear disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-tubulin antigen; inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide
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                                                                                                                     50000 BP;
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                                                      Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: AAT42752
                                                                                                                                                                                                                                        sequence encodes a beta-tubulin antigen. The protein of the membranous structure of the inner ear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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AAA64139
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                                       3.154
66.667
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                                                                 Length:
                                                                                                                      9526 G;
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                                                                                                                      other;
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Align seg 1/1

to:

AAA64139

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seq_documentation_block:
ID AAK70780 standard; DNA; 37783 BP.
XX
AC AAK70780:
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AC AAK70780:
XX
AC AAK70780:
XX
AC AAK70780:
XX
DT 06-NOV-2001 (first entry)
XX
Human immune/haematopoletic antigen
XX
Human immune/haematopoletic; immu
XX
Human; immune; haematopoletic; immu
XX
Human; immune; haematopoletic; immu
XX
Homo sapiens.
XX

PN W0200157182-A2.
XX

AC PEB-2001; 2001W0-US01354.
PR 10-MAR-2000; 2000US-0119065.
PR 04-PEB-2000; 2000US-01190668.
PR 24-FEB-2000; 2000US-018668.
PR 24-FEB-2000; 2000US-018668.
PR 14-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-025515.
PR 11-MAR-2000; 2000US-025515.
PR 28-JUN-2000; 2000US-0216647.
PR 28-JUN-2000; 2000US-0216647.
PR 28-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0225213.
PR 11-JUL-2000; 2000US-0225267.
PR 11-JUL-2000; 2000US-0225276.
PR 11-JUL-2000; 2000US-0225277.
PR 11-JUL-2000; 2000US-022527.
PR 11-JUL-20
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||||||||||:::|||
5449 AGGAGAAGGAGAAGAAG 5465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5411 GAAGGAGGAG.....AAGGAGAAGGAGGAGAAGGAGAAGGAGA 5448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO: 25592
    14 - SEP - 2000:
14 - SEP - 2000:
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21 - SEP - 2000:
25 - SEP - 2000:
25 - SEP - 2000:
26 - SEP - 2000:
27 - SEP - 2000:
29 - SEP - 2000:
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2000US-022344

2000US-0223441

2000US-0231413

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2000US-0231413

2000US-0232381

2000US-0232391

2000US-0232391

2000US-0234291

2000US-02343836

2000US-0244621

2000US-0246613

2000US-02469210

2000US-0249210

2000US-0249211
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alignment_scores:
Quality:
Ratio:
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US-08-973-363-14 x AAK70780/rev
                                                                                                                                                                                                                                                                                                 cc amino acid sequences given in AAM82170 to AAM81921. (1) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnosis and ct treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased cexample, they may be used to treat disorders associated with decreased cexample, they may be used to treat disorders associated with decreased cexample, they may be used to production of (I) additionally. (I) crossion by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally. (I) corrections may be used to produce the secreted (I), by inserting che polynucleotides may be used to prevent, correction. (I) proteins and polynucleotides may be used to prevent, corrects and cancer metastases of haematopoietic-derived cells. AAK64703 corrects and cancer metastases of haematopoietic derived cells. AAK64703 corrected from the present inmune/haematopoietic antigen genomic corrected to account the present invention. AAK54942 to AAK5950 and AAM82169
                                                                              Align seg 1/1
                                                                                                                                                           Percent Similarity:
                  16327
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01-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen useful for preventing, diagnosing and/or treating cancers metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                        Sequence 37783 BP; 9418 A; 9546 C; 9545 G; 9274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK54951 to AAK64702 encode the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                       represent sequences used
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                              7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs
               CA,
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2000US-0249215
2000US-0249217
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2000US-0249244
2000US-0249245
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2000US-0249297
2000US-0249297
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Gaps:
Identity:
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16227
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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04-FEB-2000;
24-FEB-2000;
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07-JUN-2000;
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22-AUG-2000;
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28-JUN-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                     Quality: 81.00
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17-NOV-2000;
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                      Sequence 37783 BP; 9418 A; 9546 C; 9545 G; 9274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 31437; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen
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                                 23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
                                                                                                          7 LyshisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
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XX O9-AUG-2001; 2000US-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37783 BP; 9418 A; 9546 C; 9545 G; 9274 T; 0 other;
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17

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ABA46373; STANDART; DNA; 420 BP XX

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XC ABA46373;

XX ABA46373;

XX O1-FEB-2002 (first entry)

DE Human breast cell single exon XX Human; microarray; single exon XX Human; microarray; single exon XX OS Homo sapiens.

XX O9-AUG-2001; 2001WO-US00662.

XX O9-AUG-2001; 2001WO-US00662.

XX O4-FEB-2000; 2000US-0018408.

PR 26-MAY-2000; 2000US-0603468.

PR 30-JUN-2000; 2000US-0632366.

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PR 21-SEP-2000; 200US-024263.

PR 21-SEP-2000
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                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon concleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical expression of ells. The microarray of this invention presents a far greater than expressed sequence tag microarrays. The method is suitable for than expressed sequence tag microarrays. The method is suitable for crapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. On the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly form MIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human breast cell single exon nucleic acid probe #5068
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                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                       79.00
2.469
71.111
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from:
                                                                                                                                                                          Length: 45
Gaps: 2
Percent Identity: 42.222
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to: 420
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alignment_block:
US-08-973-363-14 x
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                                                                                            alignment_scores:
 Align seg 1/1
                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block
                                                                                                                                                   Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                        fetal liver. The present probe of the invention.
                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2002
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                                                                                                                                 Sequence 420
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                                                                                                                                                                                                                                                                                                                                                          SG,
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                                                                                                                                                                                                                                                                          ۲.
                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid p
zing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foetal liver single exon nucleic acid probe #5244.
                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                          SEQ
                                                                       Ratio:
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                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
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6
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-02346359.
; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
  ABA56939
                        ABA56939
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                                                         79.00
2.469
71.111
                                                                                                                               157 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression; single exon nucleic
                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                               42 C; 122 G;
                                                                                                                                                                                                    sequence is a single exon nucleic acid
from:
                                                           Percent
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Identity:
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                                                                                                                                                                             did not form part
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2. 222
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                                                                                                                                                                                                                                                                                                            useful
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alignment_scores:

Quality:

79

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Length:

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seq_documentation_block:
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                                                              e.g. cardiovascular disease, congenital heart disease. Note: The sequence data for t
                                                                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems.
Sequence
                                                   specification,
                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                              Single
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene
cardiovascul
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27-SEP-2000;
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                                  ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                              exon
 420 BP;
                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                  Hanzel
                                                                                                                                                                                                                                                                                                              nuclèic acid
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                              IJ
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2000US-0207456
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                                                  but was obtained in electronic
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 157
                                                                                                                                                                                                                                                        5017; 530pp;
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Α,
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42
                                                                    for this patent did not form
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c;
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                                                                                                      hypertension, cardiac arrhythmias
 122
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ension; cardiac
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 99 T;
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iac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human heart cell sample
 other;
                                                                                                                                                                                                                                                                                                              gene
                                                   format
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                                                  part of the printed directly from WIPO
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                                                                                                                                                                                                                                                                                                              ij
                                                                                                      and
                                                                                                                                                                                                                                                                                                              human
                                                                                                                    system
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seq_documentation_block:
ID AAK05034 standard; DNA; 420 BP
XX
AC AAK05034;
XX
O5-NOV-2001 (first entry)
DT 05-NOV-2001 (first entry)
XX
Human brain expressed exon; g
Human brain expressed exon; g
KW Human; brain expressed exon; g
KW Human; brain expressed exon; g
KW Human; brain expressed exon; g
KW Microarray; Alzhelmer's diseas
KW epllepsy; cancer; ss.
XX
OS HOMO sapiens.
XX
OS HOMO sapiens.
XX
O9-AUG-2001; 2001WO-US00667.
XX
O9-AUG-2001; 2000US-0508408.
PN 09-AUG-2000; 2000US-0532365.
PR 26-MAY-2000; 2000US-0532365.
PR 27-SEP-2000; 2000US-05323639.
PR 04-CCT-2000; 2000US-05323639.
PR 04-CCT-2000; 2000US-02323639.
PR (MOLE-) MOLECULAR DYNAMICS INC
XX
PD Penn SG, Hanzel DK, Chen W,
XX
PP Penn SG, Hanzel DK Chen W,
XX
WPI; 2001-483446/52.
XX
XX
CM PFI; 2001-483446/52.
XX
XX
CM PFI 2001-483446/52.
XX
XX
CC The present invention provides
CC Which may enable the diagnosis
CC diseases such as Alzhelmer's of
CC thrain. They can be used to mea
CC Which may enable the diagnosis
CC diseases such as Alzhelmer's of
CC invention.
XX
X Sequence 420 BP; 157 A; 42 C;
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US-08-973-363-14 x ABA26551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
                                                                            The present invention provides a number of single exon nuclaic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the probes of the probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; microarray; Alzheimer's disease; multiple sclerosis; se epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                Example 4; SEQ ID NO: 5025; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain expressed single exon probe SEQ ID NO: 5025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 AGGAGAAGGAGGAGGAAATGAGAAGGAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 GGAGGAGAAGGAAGGATGAGAAGAA......AACAAGAAGAGGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 ATAAACTTACGTGATCCTCATTTCAAGGAGAAGAAGGAGGAGAAGTTGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
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71.111
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         G;
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5
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Identity: 42.222
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         99 T; 0 other;
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schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                  human
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seq_documentation_block:
ID AAK30564 standard; DNA; 420 BP.
XX
AC AAK30564;
XX
Human bone marrow expressed exon microarray; cancer; leukaemia; ly XX
Human bone marrow expressed exon KW
Human; bone marrow concer; leukaemia; ly XX
AC SERP-2000; 2000US-0200668.
XX
AC AAK30564; 2001; 2001WO-US00668.
XX
AC AAK30564; 2000; 2000US-020468.
AC AAC-EEB-2000; 2000US-020468.
AC AAC-EEB-2000; 2000US-023468.
AC
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Quality:
Ratio:
Percent Similarity:
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US-08-973-363-14 x AAK05034
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                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 AGGAGAAGGAGGAGGAAAATGAGAAGGAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 ATAAACTTACGTGATCCTCATTTCAAGGAGGAAGAAGGAGGAGTTGAAGAA 277
                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 GGAGGAGAAGGAGGATGAGAAAA.
                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 5121; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluLysArgGluThrLysGluLysGluAsnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG 34
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2.469
71.111
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Gaps:
Percent Identity: 42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
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                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                           English
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A; 42 C; 122 G;

99 Τ;

0 other;

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seq_documentation_block:
ID AAI15181 standard;
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US-08-973-363-14 x AAK30564
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                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
 specification, at ftp.winc in
                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
            expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer; ss.
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                                                                                                                                                  Claim
                                                                                                                                                                           analyzing
                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG
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ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGAGAAGGAAGGATGAGAAGAAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAAACTTACGTGATCCTCATTTCAAGGAGAAGAAGGAGAAGTTGAAGAA
                                                                                                                                                                                                                  2001-488901/53.
                                                                                                                                                                                                                                            SG,
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                                                                                                                                                                        genome-derived single exon nucleic acid probes useful : zing gene expression in human cervical epithelial cells
                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #5114 for
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                                                                                                                                              SEQ ID No 5114; 487pp; English.
                                                                                                                                                                                                                                          Hanzel DK,
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                                                                                                                                                                                                                                                                                            2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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2.469
71.111
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                                                                                                                                                                                                                                         Chen W,
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Gaps: 2
Percent Identity: 42.222
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cell sample.
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gene
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alignment_block:
US-08-973-363-14 x
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XX
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAI15181
                                                                                                                                                                 03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                          Human genome-derived single exon nucleic acanalyzing gene expression in human placenta
                                                                                                       WPI; 2001-488897/53.
                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                 genetic
                                                                                                                                                                                                                                                                                                                           Probe #5195
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                                                                                                                                                                                                                                                               WO200157272-A2
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              AAI36509
                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                          Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAAACTTACGTGATCCTCATTTCAAGGAGAAGAAGGAGAAGTTGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGAGAAGGAAGGATGAGAAGAAA......AACAAGAAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                 disorder;
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                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                           SEQ
                                                                                                                       Hanzel
                                                                                                                                                                                                                                                                                                                           used
                                                                                                                                                                 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                              2001WO-US00663
                                                                                                                                                         2000GB-0024263.
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2.469
71.111
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                                                           No 5195;
                                                                                                                       DK,
                                                                                                                                                                                                                                                                                                                         to measure gene expression
                                                                                                                                                                                                                                                                                                          human;
                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                          654pp; English.
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: Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                    probes
                                                                                     useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
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The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes as for antenatal diagnosis of human genetic disorders.

invention relates to single exon nucleic acid sequence is one such probe. The probes are use

probes

are tor gene (SENP)

useful

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alignment_block:
US-08-973-363-14 x AAI36509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02359.
04-OCT-2000; 2000GB-0024263.
The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 420 BP;
                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 4912; 322pp; English.
                                                                                                                                                                                                                                                                                                                              Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2001; 2001WO-US00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; human; breast disease; breast cancer; development disorder; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #4912 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 AGGAGAAGGAGGAGGAAAATGAGAAGGAGAAGAAG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
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Percent Identity: 42.222
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       PRESENTATION OF SERVICE STATES OF SERVICE SERV
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                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0207456; 30-JUN-2000; 2000US-0608408; 03-AUG-2000; 2000US-0632366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-023459; 04-CCT-2000; 2000GB-0024263;
   Claim 1; SEQ ID NO 2160; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:ABA43465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human breast cell single exon nucleic acid probe #2160.
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Gaps: 2
Percent Identity: 42.222
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C The invention relates to a spatially-addressable set of single exon concleic acid probes for measuring gene expression in a sample derived from human breast and ET 4/4 cells. The method involves contacting control of the probes with a collection of detectably labelled nucleic acids control of the probes with a collection of detectably labelled nucleic acids control of the probes are useful for concode proteins. They are useful for gene discovery, and for concode proteins. They are useful for gene discovery, and for concode proteins. They are useful for assessing the toxicity of chemical cayents on cells. The microarray of this invention presents a far greater content of the expression analysis is useful for assessing the toxicity of chemical cayents on cells. The microarray of this invention presents a far greater content sequence is a single exon nucleic acid probe of the invention. On the expression and for this patent did not form part of the content of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

**So Sequence 452 BP; 168 A; 47 C; 130 G; 107 T; 0 other;

alignment_scores; Ouality: 71.111 Percent Identity: 42.222

alignment_block: Useful out as obtained in electronic format directly sequences is a single exon nucleic acid probe of the invention. The caption of the invention of the content is an electronic format directly is sequence. The caption of the content of the con

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gb_est1:AI812274
gb_est2:BG295549
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Sequence
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Database: EST
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Query: US-08-973-363-14
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                                                                                                                                                                                                                                                                                                                       gb_est1:AW387264
gb_gss:BH055497
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gb_est2:BF239967
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gb_est1:AA699918
gb_est2:BM015597
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Database length: -1841457050
Search time (sec): 4390.400000
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-DB-EST -QFMT=48stap -SUFFIX=p3n.rst -GAPGP=11.000 -GAPEXT=4.000
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-QGAPEXT=0.050 -XGAPCP=10.000 -XGAPEXT=0.500 -FGAPCP=6.000
-GGAPEXT=7.000 -YGAPCP=10.000 -YGAPEXT=0.500 -FGAPCP=6.000
-BLEXT=7.000 -YGAPCP=10.000 -YGAPEXT=0.500 -BLDCP=5.000
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-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0
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-MINLEN=0 -MAXLEN=2000000000 -USER=US0897365_ECR1.1_2938
-NCPUG-5 -LOFUG-5 -LOGLOG -DEV_TIMEOUT=120 -MARRN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
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gb_est2:BF974760
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gb_est2:BG847842
gb_gss:CNS02VZT
gb_est2:BG026974
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AUTHORS
TITLE
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 108
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430 bp mRNA linear EST 01-DEC-1999
qh81f02.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 429.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 430)
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AI242163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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reverse of: AI242163
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                                                                                                                                                                                                                                                          constructed by Bento Soares and M.Fatima Bonaldo." 89\ c \qquad 50\ g \qquad 180\ t
                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: Pac I; Site_2: Eco RI;
/nis is a subtracted version of the original Soares fetal
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library let strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:1851099"
                                                                                                            159.00
4.077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                          86.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="20 week-post conception fetus"
                                                                               Length: 45
Gaps: 0
Percent Identity: 68.889
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from: 1
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                                                   alignment_scores:
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             Ratio:
Percent Similarity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyGluLysArgGluThrLysGluLysGluAsnLys 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 456)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptce,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                           /dev_stage="20 week-post conception fetus"
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/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
159.00
4.077
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/clone="IMAGE:435311"
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/db_xref="GDB:1335080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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86.667

Percent Identity: 68.889

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US-08-973-363-14 x AA699918/rev
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                                                    Align seg 1/1 to: BM015597 from: 1 to: 677
                                                                                                        US-08-973-363-14 x BM015597
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                                                                                                                                                                                    Percent Similarity:
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1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
                                                                                                                                                                                                             Quality:
Ratio:
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BM015597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999
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                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5417887"
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/tissue_type="mammary adenocarcinoma, cell line"
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/note="Organ: berasty vector: pcMV-spORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
ste_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 92 c 153 g 127 t
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/db_xref="taxon:9606"
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LOCUS AI890775
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                                                                   Align seg 1/1 to reverse of: AI890775 from: 1 to: 547
                                                                                                                                                                                       Percent Similarity:
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TITLE
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1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    547 bp mRNA linear EST 07-MAR-2000 wm95fll.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDL_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 ; mRNA Sequence.
                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq primer: -40UP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html

Insert Length: 1924 Std Error: 0.00
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
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                                                                                                                                                                                                                                                                                                                                                                 114 a
                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
                                                                                                                                                                                       154.00
4.053
86.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2443725"
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adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Percent Identity: 68.182
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132 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAATTAAAACAGAAAG 83

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SOURCE
ORGANISM
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US-08-973-363-14 x BF239967
                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
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LOCUS BF239967
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TITLE
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  234
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                   1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est2:BF239967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF239967 821 bp mRNA linear EST 14-NOV-2 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4133129"
/clone_lib="NIH_MGC_54"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DHIOB (Tl phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_l: Sfil (ggcgcctgggc); Site_2: Sfil (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5; and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5; CACGGCCATTATGGCC-3; and 3; adaptor sequence: 5; CACGGCCATTATGGCC-3; and 3; adaptor sequence: 5; CACGGCCATTATGGCC-3; and 3; adaptor sequence: 5; CACGGCCATTATGGCC-3; and 3; adaptor sequence: 5; CACGGCCATTATGGCC-3; and 3; adaptor sequence: 5; CACGGCCATTATGGCC-3; and 3; adaptor sequence: 5; ATTCTAGAGGCGGACACATG-dT(30)BN-3; (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
45 a 149 c 190 g 137 t
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                                                                                                          BF239967
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3.744
84.783
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/db_xref="taxon:9606"
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alignment_block:
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LOCUS AW387264
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                                                                                                                                                                                                                                                              Percent Similarity:
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TITLE
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                                                                   159 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 AGACCAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCA 333
                      17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG
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  gb_est1:AW387264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=wR1&t2=MR1-ST0088-
101199-003-b09&t3=1999-11-10&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                         Quality:
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MR1-ST0088-101199-003-b09
AW387264
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Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCGP http://www.ludwig.org.br/ORESTES The FAPESP/LICR Human Cancer Genome Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                       reverse of: AW387264
                                                                                                                                                                                                                                                                                                                                                                                                               tissue mRNA and cDNA amplification were performed under low stringency conditions." 52\ c \qquad 41\ g \qquad 104\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                              128.00
3.459
82.222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Adult"
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REFERENCE
AUTHORS
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VERSION
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US-08-973-363-14 x BH055497
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                        140
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                                        7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
                      AAGCAAAGAGGAAGCACAAGCAAAGAGAACTCAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chorl.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tub/bac_ends/mouse/bac_end_intro.html
Plate: 278 row: I column: 16
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C. M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-278I16.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPCI-24-278I16.TJ RPCI-24 Mus
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 653)
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                                                                                                                                                                                                                                                                                                                                 255
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301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-278I16"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                            /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Stre_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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3.333
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Gaps: 0
Percent Identity: 51.282
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Mus musculus
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LOCUS BF068827
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BF068827
BF068827.1 GI:10845778
Quality:
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Length:

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LOCUS BG790466
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US-08-973-363-14 x BF068827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, 17el: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537 bp mRNA linear EST 29-NOV-2001 sae69h05.yl Gm-c1064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1064-3801 5' similar to TR:003982 003982 HYPOTHETICAL 19.8 KD PROTEIN. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4453 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae; Phaseoleae;
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Glycine max
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BG790466.1 GI:14126028
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/note="Tector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The cDNA library was constructed from mRNA isolated from the epicotyls of 2 week old seedling for the cultivar Williams. The seedlings were germinated in a growth chamber, excised above the soil level, and the plants were placed in a 100 ppm solution of auxin for 24 hours prior to harvesting. Complementary DNA was synthesized
                                                                                                                                                                                               /tissue_type="seedling epicotyls"
/dev_stage="2 week old"
                                                                                                                                                                                                                                             /clone="GENOME SYSTEMS CLONE ID: Gm-c1064-3801"
/clone_lib="Gm-c1064"
                                                                                                                                                                                                                                                                                           /cultivar="Williams"
/db_xref="taxon:3847"
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Percent Identity: 46.667
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alignment_block:
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Email: 1-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. Foor further information
call: (800) 430-0030 or (314) 427-322 FAX:(888) 919-3324 or (314)
427-3324 or contact:clones@genomesystems.com or info@genome
ystems.com web site:www.genomesystems.com
Seq primer: 5. TITTTTTTTTTTTTTTTT(A/C/G)-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 796)

Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genemics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                 Contact: Vodkin, L.O., PI, A Functional Genomics Program Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_ESTs: AW277969 corresponding to Gm-c1019-3195 (5')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GM700017B10E2 Gm-r1070 Glycine
                                                                                                                                                                                         Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                            University of Illinois Edwin R. Madigan Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core euRosidae; eurosids I; Fabales; Fabaceae; Papilionoidea
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                                                                                                                                                                                                                                                                                                                      Lewin, H. A., Director,
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2.672
71.111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
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                                                                                                                                                                                                                                                                                                                           Keck Center for Comparative and Functional
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                                                                                                                                                                                                                                            Gregory,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   edons; core eudicots;
Papilionoideae; Phas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                               IL 61801,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Lewin, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coryell, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phaseoleae;
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seq_name: gb_est1:BE211196
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US-08-973-363-14 x BE822468/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS BE211196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: BE822468 from: 1 to: 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 ysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAGGATGAGAAGAAG
                                                             Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Ratio:
       1 (bases 1 to 294)
Shoemaker,R., Keim,
                                                                                                                                                                                                                                                                                                                                                                    HE211196 294 bp mRNA linear EST 04-DEC-2001 SO58b05.y1 Gm-c1039 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-c1039-2194 5' similar to TR:003982 003982 HYPOTHETICAL 19.8 KD
                                                                                                                                                                                                                                                                                                              PROTEIN. ;, mRNA sequence BE211196
                                                                                                                                                                                                                                                   BE211196.1 GI:8827466
EST.
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//db_xref="taxon:3847"
//clone="dm:1070-6747"
//clone_lib="Gm:1070-6747"
//clone_lib="Gm:1070"
//note="The library Gm:1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,700 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm:1070. The cDNA clones of the reracked to form library serve then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.unm.edu/ResearchFrojects/Soybean/index.html. Reracking was performed by Genome Systems, 5t. Louis, http://www.genomesystems.com, and 3' sequencing by the keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm:1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of 'OTHER EST'."

274 t 30 others
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2.897
74.359
   Keim, P., Vodkin, L.,
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Gaps: 1
Percent Identity: 48.718
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Erpelding, J., Coryell, V., Khanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 others
                                                                                              Phaseoleae;
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BASE COUNT ORIGIN

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

DEFINITION

539

SOURCE

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TITLE
JOURNAL
COMMENT
DEFINITION sh95908.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-7959 5' similar to TR:003982 003982 HYPOTHETICAL 19.8 KD PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-973-363-14 x BE211196
                                                                                                                                                                                           seq_name: gb_est1:AW459832
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ORIGIN
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                                                                                                                                                                                                                                                             128
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                                                                                                                                                                                                                                                                                                                                                                            90 AGAGCCT.....AAGAAAGAAGAAGAAGAAGAAGAAGAAGACAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 GAGGAGCCAAAGAAGGAGGGTGAAGCCAAAAAGGAAGAGGAGAAAAAAGGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23 ::::::||| | | | | | ::: :::||||:::||||:::
                                                                                                                                                                                                                                                             AGAAAGAAGAAGAAG 144
                                                                                                                                                                                                                                                                                                             ysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkay Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1211 Std Error: 0.00
High quality sequence stop: 245.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemakor R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
//db_xref="taxxon:3847"
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//tissue_type="whole seedling without cotyledons"
//tissue_type="whole seedling without cotyledons"
//tissue_type="whole seedling without cotyledons removed at the time of harvest. The seedlings for the cultivar Ogden were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhor restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by Xhol digestion. The CDNA fragments were directionally cloned into the EcoRI xhol restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."
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2.677
79.487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
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Gaps: 1
Percent Identity: 46.154
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KEYWORDS
SOURCE
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US-08-973-363-14 x AW459832
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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     103
                                                   23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
                                                                                                            53
                                                                                                            GAGGAGCCAAAGAAGGAGGGTGAAGCCAAAAAGGAAGAGGAGAAAAAGGA 102
                                                                                                                                                                LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further informatical: (800)-533-4363 or contact via email: ccu@resgen.com Seq primer: -40RP from Gibco High quality sequence stop: 399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nhoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                                                                                                                            AW459832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

74 c 109 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
                                                                                                                                                                                                                                                                                                                                                             83.00
2.677
79.487
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AAGAAAGAAGAAGAAGAAGAGACAA 140
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Percent Identity: 46.154
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BASE COUNT
ORIGIN
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US-08-973-363-14 x AL628267
seq_name: gb_gss:AG173980
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                                      380 AAAAGGACCCTAAGAAAGAAAAGAAG 405
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                                                                                                                                      26 uIleGlyIleLysLysGluAlaGlyGluLysArgGluThrLysGlu....
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                                                                                                            Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST
TROPICALIS_SEQUENCE_ID: TGAS00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Huckle E
Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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2.767
71.429
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/lab_host="Escherichia coli XII-blue"
/note="vector: pcS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
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/db_xref="taxon:8364"
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LOCUS AG173980
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Ratio: 3.154 Gaps: 0
Percent Similarity: 74.286 Percent Identity: 54.286
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Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical submitted (102-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: RP43-044B16.TJ, genomic survey
sequence.
AG173980
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BAC end sequences of Library RPCI-43
Unpublished
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-044B16.TJ
Pan troglodytes
Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="lymphocytes"
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, 380 c 93 g 407 t 15 others
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                                    Patent: WO 9639505-A 2 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1 . 153
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1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                     A58683 1.53 bp
Sequence 2 from Patent W09639505.
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37 c 27 g 28
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AC0214624 Homo sapi
AC021464 Homo sapi
AC021211 Homo sapi
AC022121 Homo sapi
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AC106437 Homo sapi
AS8685 Sequence 30
AF1004397 Gallus ya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAAAAGAGAGCTCAGAGACTTTGTGGTGCG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse DNA-binding protein L10410 x66028 L10410.1 GI:455014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                        IAHSNOKSAAGLPDYYCKWQGLPYSBCSWEDGALISKKFOTCIDEYFSRNOSKTTPFK
DCKVLKRPRFVALKKOPSYTGGHEGLELRDYGLNGLNWLAHSWCKGNSCILADEMGL
GKTIOTISFLRVLFHEBDLYGFFLLVVPLSTLTSWQRELDTWASOMNAVVLGDINSR
GKTIOTISFLRVLFHEBDLYGFFLLVVPLSTLTSWQRELDTWASOMNAVVLGDINSR
UMIRTHEWMHPQTKRLKFNILLTTYEIILLKDKAFLGGLNWAFIGVDEAHRLKNDDSLL
YKTLIDFKSNHRLLITGTPLONSIKELMSLLHFIMPEKFSSWEDFEEEIGKGREYGYA
SLHKELEFFLLRVKKOVEKSLPAKVEÖILKEWSALDGVYYKWILTRNYKALSKGSY
SSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALOHLIRSSGKLIILLDKLLIRL
                                                                                                                                                                                            SQSGSSDSDSGSDSGSQSESESDTSRENKVQAKPPKVDGAEFWKSSPSILAVQRSAML
RKQPQQAQQQREASSNSGSEEDSSSSEDSDSSSGAKRKKHDEDWQNSGSSGSPSQLG
SDSESEEERDKSSCEDFESDYEPKNKVRSKKPQNRSKSKGKKILGQKKRQIDSSEDE
DDEDYDNDKRSSCROFTESDYEPKNKVRSKKPQNRSKSKGKKILGQKKRQIDSSEDE
DDEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEYCGEDVPQPEDEEFETIERVM
DCRVGRAKGATTIYAVEADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
TLKQQKTAAKTENYKKKDOFTKRWLKNASPEDVEYYNCQQELFUDDLHKQYQIVERI
RERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDF
CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKG
                                                                                                                                                                                                                                                                                                                                                   /product="DNA-binding protein"
/protein_id="AAB08486.1"
/db_xref="GI:455015"
                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CHD-1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="plasmacytoma"
1. .5349
                                                                                                                                                                                                                                                                                                                                    translation="MNGHSDEESVRNGSGESSQSGDDCGSASGSGSGSSSSGSSSDGSS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CHD
171. .5306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CHD-1"
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AR029026
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AF006513
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AR029026
AR029026.
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54; Conserv
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5947) Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1311)
de Lange, T., Steensel, Bvan. and Bianchi, A.
Altered telomere repeat binding factor
Patent: US 5859183-A 3 12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
Unclassified.
                                                                                                                                                    AF006513.1
                                                                                              Homo sapiens
                                                                                                                                                                       Homo sapiens CHD1 mRNA, AF006513
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DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSGTERAGGRLGKVKGPTFRISG
VQVNAKLVIAHEDELIPLHKSIPSDPEERKQYIPICHTRAHFDIDMGKEDDSNLLIG
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QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEXSDEDDDKLNDSKPESK
DRSKKSVVSDAPVHITAGGEPVPIAESSBELDQKTFSICKERMEPVKAALKQLDRPEK
GLSERGOLEHTRQCLIKIGDHITECLKEYSNPEDIKOKRLMIFVSKFTEFDARKH
KLYKHAIKKRQESQQNSDQNSNYATTHYIRNPDMERLKENTNHDDSSRDSYSSDRHLS
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QYHDHHADRHOGDSYKKSDSKRAPYSSSNGKDHREMDHYRDDSSRDSYSSDREKHRKLDID
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257 c 316 g
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HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT®
1067 c 1319 g 1224 t
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                                                                                                                                                      GI:2645428
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100.0%;
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Pred. No.
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Pred. No. 2.1e-48;
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US 5859183.
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SOURCE
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AC092372/c
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                               AC092372 101
Homo sapiens chromosome 5
AC092372
AC092372.3 GI:17402768
HTG.
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97470991
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27; Conservative
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//PIOCHIL 1d**AB87381.1*
//PIOCHIL 1d**AB97381.1*
//PIOCHIL 1d**AB87381.1*
//PIOCHIL 1d**AB97381.1*
//PIO
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/db_xref="taxon:9606"
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Pred. No.
                                                                                             101220 bp DNA 1
ne 5 clone RP11-58M12,
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                                                                                                linear PRI 07-DEC-2001, complete sequence.
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DOE Joint Genome Institute.

S DOE Joint Genome Institute.

S DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, I to 134365)

E 3 (bases I to 134365)

S DOE Joint Genome Institute and Stanford Human Genome Center.

L Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

E 4 (bases I to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                               Human.
Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134355)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
MOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-7UL-2001) Production Sequencing Facility, DOE Joint Submitted (03-7UL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 witchell Drive, Walnut Creek, CA 94598, USA

(Dases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 witchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC012624 134365 bp DNA linear PRI 21-JUL-
HOMO Sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624 AC012624.6 GI:14993679
HTG.
                                                                                                                                                                                                                                                                                     Unpublished
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DOE Joint Genome Institute.
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Similarity 100.0%;
27; Conservative
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18862 c 17827 g 30409
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/db_xref="taxon:9606"
/chromosome="5"
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Pred. No.
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Institute, 2800 Mitchell

, DOE Joint A 94598, USA

USA

Euteleostomi; Homo.

PRI 21-JUL-2001

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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Perreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Plerre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Dienter, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
                                                                                                                                                                                                                                              Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 143079)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-58M12
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                          Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5154
Center clone name: 58_M_12
                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center
                                                                                                                                        Web site: http://www-seq.wi.mit.edu
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24497 c 25503 g 43951 t
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Summary Statistics
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                      43971
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46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp
51831 51930: gap of 100 bp
51831 51930: gap of 100 bp
51831 62619: contig of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38821 38920: gap of 100 bg
38921 40411: contig of 1491
40412 40511: gap of 100 bg
40512 43279: contig of 2768
43280 43379: gap of 100 bg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106410 106509:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62620 62719: gap of 100 bp 62720 75408: contig of 12689 bp in length 75409 75508: gap of 100 bp 75509 92516: contig of 17008 bp in length 92517 92616: gap of 100 bp 92617 106409: contig of 13793 bp in length
                      a
                                            clone_end:T7
vector_side:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:left"
38921...40411
                                                                                                           /note="assembly_fragment"
106510. .143079
                                                                                                                                                     92617.
                                                                                                                                                                                                75509.
                                                                                                                                                                                                                                          62720.
                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
51931. .62619
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                                                                                                                                                                                                                                                                                                                                                                                                                40512.
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                                                                                  /note="assembly_fragment
                                                                                                                                                                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-58M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                  /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                          'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11 Human Male BAC"
                      26246 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .143079
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20: gap of 100 bp
                                            _side:right"
                                                                                                                                                                                                .92516
                                                                                                                                                                                                                                          .75408
                                                                                                                                                                                                                                                                                                                                                                                                                  .43279
                                                                                                                                                                                                                                                                                                                               .51830
                                                                                                                                                                                                                                                                                                                                                                        .46905
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                 26678 g 45278 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp
contig of 10689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 36570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                      906 others
```

Query Match

17.6%;

Score 27;

DB

2;

Length 143079;

Best Local

Similarity

0;

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Db 116192 CAGACCCGTGCAGACTACCTCATCAAA 116218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 CAGACCCGTGCAGACTACCTCATCAAA 102
                                                                                                               Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 142744 bases at least Q20
Consensus quality: 142744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation.

**NOTE: This is a 'working draft' sequence. It currently

**consists of 7 contigs Gaps between the contigs

**are represented as runs of N. The order of the pieces

**is believed to be correct as given, however the sizes

**of the gaps between them are based on estimates that have

**provided by the submittor.*

**This sequence will be replaced

**by the finished sequence as soon as it is available and

**the accession number will be preserved.

**100975 100974: contig of 56174 bp in length

**56175 56274: gap of unknown length

**113128 100974: contig of 44600 bp in length

**113128 113270: gap of unknown length

**11328 113291 113290: gap of unknown length

**11328 113291 113994: gap of unknown length

**11328 113991: contig of 1404 bp in length

**11328 113991: contig of 3503 bp in length

**113291 113991: contig of 3503 bp in length

**113391 113991: contig of 3503 bp in length

**113391 11390: contig of 3503 bp in length

**113391 11390: contig of 3503 bp in length

**113392 113991: contig of 3503 bp in length

**113951 11390: contig of 3503 bp in length

**113951 11390: contig of 3503 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Project Information
Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Direct Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14555)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Joint Genome Institute
Center Code: JGI
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC008531.3 GI:12830078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 0;
                                                                                                Location/Qualifiers
           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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VERSION
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AC091946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Cuality coverage: 5.38 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
* NoTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are trepresented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC091946 193446 bp DNA linear HTG 09-JUN-2001 HOMO Sapiens chromosome 5 clone RP11-360I2, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
AC091946
                                                                                                                                                                                                                                                                                                                                             * as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center Project Name: 544799
Center clone name: RPCI-11_36012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (09-UN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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27; Conservative
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                                                                                                                                 1359
1459
2668
2768
3824
3924
1358: contig of 1358 bp in length
1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1097 bp in length
6020: gap of unknown length
7494: contig of 1474 bp in length
7594: gap of unknown length
7594: contig of 1502 bp in length
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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FEATURES

source

REFERENCE AUTHORS TITLE JOURNAL

SOURCE ORGANISM

Homo sapiens Eukaryota; M

KEYWORDS VERSION ACCESSION DEFINITION

REFERENCE

Unpublished

AUTHORS TITLE JOURNAL

COMMENT

RESULT AC008531

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                                                                                                                                                                                                               BASE COUNT
ORIGIN
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                                                                                                                 Query Match
Best Local
                                                                                             Matches
  87703
                                                                                                                                                                                                                                                                                                                                                                                  source
                                            76 CAGACCCGTGCAGACTACCTCATCAAA 102
CAGACCCGTGCAGACTACCTCATCAAA 87729
                                                                                                                 Similarity
                                                                                                                                                                                                                                        57571
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117572
117672
1137673
123739
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130584
130684
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102895
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79796
79896
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/db_xref="taxon:9606"
/chromosome="5"
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1. .193446
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27563: contig of 3948 bp in ler
27663: gap of unknown length
30987: contig of 4978 bp in ler
31087: gap of unknown length
40978: contig of 4978 bp in ler
36165: gap of unknown length
41078: gap of unknown length
45663: contig of 4985 bp in ler
45763: gap of unknown length
45643: contig of 5992 bp in ler
45763: gap of unknown length
57359: contig of 5914 bp in ler
51845: gap of unknown length
67981: gap of unknown length
67981: gap of unknown length
67981: gap of unknown length
74132: contig of 61912 bp in ler
74232: gap of unknown length
74232: gap of unknown length
79795: contig of 5563 bp in ler
74232: gap of unknown length
102794: contig of 5615 bp in ler
102794: contig of 7616 bp in ler
102794: contig of 9903 bp in ler
102894: gap of unknown length
102794: contig of 6605 bp in ler
117671: gap of unknown length
1130833: gap of unknown length
114144: gap of unknown length
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WI-13675 G23101
SHGC-58345 G38487
SHGC-103595 G57841.
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Homo sapiens chromosome 5 clone
AC022121
AC022121.6 GI:15375145
                                      AC092382
AC092382.1 GI:14589571
HTG; HTGS_PHASE1; HTGS_DRAFT;
                                                                                276181 bp
Homo sapiens chromosome 5 clone
47 unordered pieces.
AC092382
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27; Conserv
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On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (11-AUG-2001)
Drive, Walnut Creek, CA
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DOE Joint Genome Institute and Stanford Human Genome Center.
                Homo sapiens
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Quality: Phrap Quality >=40 99.8% of Sequence;
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Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2007H13"
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COMMENT

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Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 26799 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Quality coverage: 8.62 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 47 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
This record will be updated with the finished sequence.
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DOE Joint Genome Institute.
Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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1 (bases 1 to 276181)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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1161: gap of unknown length
2827: contig of 1666 bp in length
4227: gap of unknown length
4227: gap of unknown length
4327: gap of unknown length
5518: contig of 1291 bp in length
5718: gap of unknown length
5718: gap of unknown length
6933: contig of 1265 bp in length
6943: contig of 1339 bp in length
8422: contig of 1339 bp in length
8422: contig of 1249 bp in length
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Db 213649 CAGACCGGTGCAGACTACCTCATCAAA 213623
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Best Local S
Matches 27
                                                                                                               ch 17.6%; So 1 Similarity 100.0%; F 27; Conservative 0;
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                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone="$P211-75H1"
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157894: contig of 11081 bp in length
157994: gap of unknown length
171752: contig of 13758 bp in length
171852: gap of unknown length
201687: contig of 29835 bp in length
201687: gap of unknown length
201268: gap of unknown length
231268: gap of unknown length
231268: contig of 29481 bp in length
231368: gap of unknown length
276181: contig of 44813 bp in length.
                                                                                                            Score 27; DB; Pred. No. 0.0
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of unknown length
g of 8217 bp in length
if unknown length
g of 11499 bp in length
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g unknown
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g of 1994
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                                                                                                                                                                                                                                                                                                                                      Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2292)
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D14316.1 GI:391639
ORF2.
                                                                                                                                                                                                     Funahashi, J., Sekido, R., Murai, K., Kamachi, Y. and Kondoh, H. Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                             Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (Te::022-272-9499, Fax:022-272-3982)
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224
Location/Qualifiers
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                  Funahashi,J.
Unpublished (1994)
                                                                                                                                                                            Development 119 (2), 433-446 (1993)
                                                                                                                                                                                            embryogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (library: lambda gt11) 13 day embryo mRNA, clone JF11.
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/organism="Gallus gallus"
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/tissue_type="lens"
/clone_lib="lambda gt11"
/dev_stage="13 day embryo"
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/db_xref="taxon:32644"
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Other publication AU 5906996 961224
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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                                                              protein,
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LIRLREGGNRVLIFSQWVRMLDILAEYLKYRQFPDRLDGSIKGLIRGALDHENAEG
SEDECETLSTERAGGLGI LLAESADTVU FDSDWHDQNDLDAQARAHRIGOKKOVNIYRL
VTKGSVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSTPSSTPPNKEELSAILK
FGAEBLFKEPEGEEQEPCEMDLDEI LKARAFTRNEPEGFLTVGDELLSQFKVAANFSNMD
EDDIDLEPERMSRNWAEBI IPESQRRALEEEISMOLDELLSQFKVAANFSNMD
EDDIDLEPERMSRNWAEBI IPESQRRALEEEISMOLDERLSGFKDAKOSFKGS
ERRSRRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGE
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385 c 546 g 534 t
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RISGVQVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSN
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HN fragment of delta-crystallin enhancer."
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Griffiths,R. and Korn,R.M.
A CHD1 gene 1s Z chromosome linked in the chicken Gallus domesticus
Gene 197 (1-2), 225-229 (1997)
97473516
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Griffiths,R. and Korn,R.M.
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                                                                                                                                                                                                                                                                                 2446 a
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MIRTHEWMHOQTKRLKFNILLTTYEILLKDKSSTLGGLNWAFIQVDEAHRLKNDDSLLY
RTLLDPKSHRHRLLITGTPLQMSLKELWSLLHEFINDERFSSWEDFEEBHGKGRETGYAS
LHKELEPFLLRVKKDVEKSLPAKVBQILRMEMSALQKQYYKWILTRNYKALSKGSKG
STSGFLNIHMELKCCHHCYLLKPDDWSFYNKQEALQHLJRSSKGSKGKLILLDKLLIRL
REKGNRYLIFSQWFMALDILABYLKYROPFORLDGSIKGELEKQALDHFWAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKGS
VEEDILERAKKKWVLDHLVIQMADTTGKTVLHTGSTPSSSTPFNKEELSALLKFGAEE
LFKEPGGEEGDEPQENDIDEILKRAETRENEFQFLYWGDELLSQFKVANFESNMEDDIDE
LEPERNSRNWEETIPESQRRRIEBEERQKELEFIYWGDELLSQFKVANFESNMEDDIDE
LEPERNSRNWEETIPESGRRRIEBEERQKELEFIYWGDELLSQFKVANFESNMEDDIDE
LEPERNSRNWEETIPESGRRRIEBEERQKELEFIYWLPRWRKGCKOXJSFNGSEGRRSR
SRRYSGSDSDSITERKFKKRGPRTITBENIKGFSDAEIRRFIKSYKKFGGFLERLD
AVARDAELVDKSETDLERLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPFREISGV
QVNAKLVISHEEBLAPLHKSIFSDPEERKRKVIDPGTKAAHDDIDGKKEDDSLLVGI
                                                                                                                                                                                                                                                                                                                                                                                                                       SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
HRSPFEHSSDHKSTPEHTWSSRKT"
                                                                                                                                                                                                                                                                         /note="short insert found in longer variant mRNA of CHD-2"
1223 c 1520 g 1683 t
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THVIRNPDVERLKETTNIHDDSSRDSYSSDRHLSGYHDHHKDRHOGDAYKKSDSRKRPY
SAFSNGKOHRUMDHYKQDSRYYSDSKHRKLDDHRSKDHSSNLEGNILKOSRGHSDHRSH
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NKEKRENKYKESTOK EKEPKEEKVNEMKSENKEKKKIPLLDPYHITATSEPVHISE
ESEELHOKTFSYCKERMRYKAALKQLDRPEKGLSEREDLEHTROCLIKIGHITECL
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RLAGAGNSKRRKTRNKKNKMKASK I KEE I KSDSSPQPSEKSDEDDEEEDNKDE I VSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHSNOKSAAGYPDYYCKWOGLPYSECSWEDGALIAKKFQARIDEYFSRNOSKTTPFKD
CKVLKQRPRFYALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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DDDEDVDKRGSRAQATVNVSYKBAEBTYTDSDDLLEVGGEDVPGTEEDEFETIEKERD
SRIGRKGATGASTTIVAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="01:2501846"
/translation="MNGHSDEESVRNSSGESSRSDDDSGSASGSGSGSSSGSSSDGSS
SQSGSSDSESGSESGSQSEEDSTSREKKQVQAKPPKADGSEFWRSSPSILAVQRSAV
LKKQQQQQKAASSDSGSEEDSSSSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGS
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/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
/db_xref="taxon:9031"
1. .6872
                                                                                                                                                                                                                                                                                                                                                      /gene="CHD-Z"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
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Search completed: August 3, 2002, 01:42:15 Job time: 40705 sec

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                 Score
  153
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Match
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1: /SIDS1/gcgdata/
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153
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Copyright (c) 1993 - 2000 Compugen Ltd.
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153
6608
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AAT42756
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               Mouse CHD-1 gene (
Altered telomere r
Chick CHD-1A gene
Chicken CHD-1A gene
Enterococcus faeca
Chick CHD-W gene f
DNA encoding novel
Trichoderma reesei
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  encoding novel
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_		225		AAK83089	Human immune/haema
11 17	7 11.1	225	22	309	
۰, ـ		225		AAK90734	Human digestive sy
س د	11.	225	22	AAK90736	digestive
15 17	11	657	21	AAC79872	Human secreted pro
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7 1	11.	1515	20	AAX81997	meg
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1	11.	1812	24	ABI99584	Mouse ischaemic co
. 0	: 11	2694	23	ABL10922	Drosophila melanog
→	11.	21721) () ()	ABA06775	Human genomic DNA
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л≄	1:	31994	2 1	AAS20619	DNA encouring mover
σ,	10.	133	22	ABA73552	
7	10.	133	22	AAK21998	brain expre
- α	10.	133	22	AAK48161	
o vo	10.	133 133	3 6	AA153991	#226// used
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33 16	10	517	22	ABA61038	foetal :
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7	10.	653	21	AAF11160	Fusarium venenatum
- α	10.	927	22	ABA77010	Proliferative glom
9	10.	992	23	ABL18639	Drosophila melanog
40	10.	1001	21	747	
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42 L	10.	1064	200	AAX85048	secrete
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AAT42756	standard;	DNA;	153	BP.	
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misc_difference 52..81
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(ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse CHD-1 gene (bases 3855-977).
                                                95GB-0011439
                                                                                           96WO-GB01341
                                                                                                                                                                                                                      /note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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RESULT
AAV59280
ID AAV5
XX AAV5
XX AAV5
XX AAV5
XX ds;
XX telc
XX telc
XX telc
XX Synt
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Matches 153
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                                                                                               04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                        13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ageing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           telomere repeat binding factor; ageing; ataxia telangeictasia; Do
  De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                               ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 61 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
Lange
                                                                                            98US-0018628
97US-0800264
                                                                                                                                                                     98WO-US02765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76pp; English.
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..1311
                                                                                                                                                                                                                                                                                                                  /product= "A-TRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 C;
Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
Steensel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; DB 18;
4.3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-TRF; dimerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
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Qy

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Query Match
Best Local
Matches 5
                                                                                                                The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. attaia telangeictasia, Down's syndrome, attophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (Including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-diners and antibodies, use to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                Claim 14; Page 110-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW59280
                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-480769/41.
 1 Similarity 100 54; Conservative
                                                                                       1311
                                                                                       вP;
                                                                                       441 A;
                35.3%;
                                                                                                                                                                                                                                                                                                                                163pp; English.
                                                                                       257
Score 54; DB Pred. No. 1.4
0; Mismatches
                                                                                     c;
                                                                                       316
                                                                                       <u>و</u>
                                                                                       297
                  DB 19;
1.4e-17;
                                                                                     н,
                                                                                       0
                                Length 1311;
                                                                                       other;
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                                                                                                                                                                                                                                                               repeat
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RESULT
AAT42757
ID AAT4
밁
               P-PSDB; AAW08147
                                                                                                                                                                                                   Gallus
                                                                                                                                                                                                                          Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                           Chick CHD-1A gene fragment.
                                                                                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                                                                                                                    1258 aaaaaaccacaagcaaaacagttacagacccgtgcagactacctcatcaaacta 1311
                                                                        06-JUN-1995;
                                                                                                                                                                                                                   CHD-1A;
                                                                                                                                                                                                                                                                            AAT42757;
                                                                                                                                                                                                                                                                                            AAT42757
                        WPI; 1997-043127/04
                                       Griffiths R,
                                                                                        05-JUN-1996;
                                                                                                         12-DEC-1996.
                                                                                                                         WO9639505-A1
                                                                                                                                                                          misc_difference
                                                       (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                            52 AAAAAACCACAAGCAAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTA
                                                                                                                                                                                                                                                                                                           u
                                                                                                                                                                                                   qs
                                                                                                                                                                                                                   CHD-W;
                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                           (first entry)
                                                        INNOVATION
                                       Tiwari
                                                                                                                                                                                                                   Σ
                                                                        95GB-0011439
                                                                                        96WO-GB01341
                                                                                                                                                                          Location/Qualifiers 52..81
                                                                                                                                                          /note=
                                                                                                                                                                                                                   chromosome;
                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                            DNA;
                                       В;
                                                                                                                                      "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                   ss.
                                                                                                                                        translated .
Fig 3"
                                                                                                                                                 amino
                                                                                                                                                         22-51
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Avian chromodomain-helicase-DNA binding genes

determine

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FXGXSSSSSSSXS

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AAT42751
The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = AVIA1) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic
                                                                                                                                                                                                                                                                                                          Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken CHD-1A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine seex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                       Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42751 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        birds - used
                                                                                                                                                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 TACAGACCCGTGCAGACTACCTCAT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tacagacccgtgcagactacctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                          Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                         95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
228..5390
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                     В
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                 Query Match
Best Local :
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l Similarity 22; Conserv

14.4%; ilarity 100.0%; Conservative

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Mismatches

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Gaps

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Score 22; Pred. No.

DB 20; 0.14;

Length 13884;

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AAX13278/c
                                                                           A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
Sequence 13884 BP; 4353 A; 2723 C; 2370 G; 4422 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1453-1460; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-1997;
06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX13278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-045171/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09850555-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; attenuation; computer readable medium; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis genome contig SEQ ID NO:341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX13278 standard; DNA; 13884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 TACAGACCCGTGCAGACTACCTCAT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tacagacccgtgcagactacctcat 4147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            faecalis; contig; detection; Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0046;
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13595

TGATCCTGATAAAAAACCACAA 33 |||||||||||||||||||||| TGATCCTGATAAAAAACCACAA 13574

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AAS81107
ID AAS8
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAT42758
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                             RESULT
                                                                                                 Query Match
Best Local s
Matches 20
                                                                                                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A - Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
          AAS81107 standard; cDNA; 803 BP
                                                                                                                                                     Sequence 153
                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                 Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chick CHD-W gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT42758 standard; DNA; 153
                                                                                                                                                                                                                                                                                                Avian
                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42758;
                                                            70
                                                                              70 CAGTTACAGACCCGTGCAGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                          1997-043127/04
DB; AAW08148.
                                                                                                                                                                                                                                                                                      chromodomain-helicase-DNA binding genes determine sex
                                                                                                                                                                                                                                                                 8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             дs
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                     used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-W;
                                                                                                  Conservative
                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                     INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                    for sex determn. and
                                                                                                                                                                                                                                                                                                                                                Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                        95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                     56 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                            100.0%;
                                                                                                                                                     36 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "bases 52-81 are a repeat of bases and are ignored in the translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid sequence given in Fig 3"
                                                            89
                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΒP
                                                                                                            Score 20;
Pred. No.
                                                                                                                                                     31 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss.
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                    to control sex of progeny
                                                                                                                                                     30 T; 0 other;
                                                                                                                      DB 18;
                                                                                                            5,
                                                                                                  0;
                                                                                                                      Length 153;
                                                                                                 Indels
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amino
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                                                                                                  Gaps
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RESULT AAF15189 ID AAF1 XX AC AAF1

AAF15189

standard;

cDNA;

905

ВP

밁 δÃ

26 AACCACAAGCAAAACAGTT aaccacaagcaaaacagtt 191

44

Matches

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

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Query Match
Best Local
                                                                                                                                       imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197 AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                       Sequence 803 BP;
                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS81107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #16911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food supplement;
Local Similarity hes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping; gene mapping; gene
upplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG16920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 16911; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                       221 A;
                12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang
                                                                                       195 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΥT
                  Score 19;
Pred. No.
                                                                                       240 G;
                                                                                       147 T;
                  4.8;
                                     DB
                                   23;
                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; forensic; genetic disorder; ss
                                                                                         other;
                                 Length 803;
                                                                                                                                                                                                                                                                                                                                                                                                techniques
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The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal (CC et ls. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first procession of genes from FF cells allows the production of the global expression of genes from FF cells allows the production be constituted and gene copy number variation and stability can be constituted in the expression of genes can be used to study how FF cells and the conditions of unknown open reading frames as poore CC adapt to changes in culture conditions, environmental stress, spore CC adapt to changes including elimination or catabolic pathway complemental, recombination, metabolic or catabolic pathway complements, come gene or open reading frame, and organisation of the array equals one gene or or open reading frame, and organisation of the conditions environmental stress sport on an irroarrays based on function of the gene products to facilitate consists of the constitute of the products and the products of the macroarrays based on function of the gene products of sacilitate and sport pathway and products to facilitate and products and product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 89; Page 3111; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200056762-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 905 BP; 226 A; 265 C; 185 G; 218 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrate of expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-594572/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO NORDISK BIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multiple gene expression; filamentous fungal cell; EST;
291 acagaccaaaaaaccaca 308
                                                                                           45 ACAGACCAAAAAACCACA 62
                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shuster JR, Kauppinen S, Clausen IG,
                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                       0;
                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                              DB 21; Length 905;
                                                                                                                                                                                       0;
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                                                                                                                                                                                  0;
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RESULT AAS81550

AAK83089

AAK83089 standard; DNA;

RESULT

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                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and copylopetide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques (I). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (I) and (II) are useful for treating climaging of sites expressing (II). (II) and (III) are useful on mutations in climaging of sites expressing (II). (II) and (III) are useful for mutations cresponsible for genetic disorders or other traits to assess biodiversity canditor produce other types of data and products dependent on DNA and climaging sequences and sequences of the invention.

Consideration, but was obtained in electronic format directly from WIPO at the printed sequences.
                                                                                             Matches
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 17354; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #17354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS81550 standard; cDNA; 5168 BP.
                                                                                                                                                                                                        Sequence 5168 BP; 1428 A; 1397 C; 1194 G; 1149 T;
                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002
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725 ttccagatgatcctgata 742
                        5 TTCCAGATGATCCTGATA 22
                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639362/73
                                                                                          18; Conservative
                                                                                                             100.0%;
                                                                                                             11.8%; Score 18; DB 23; Length 5168; 100.0%; Pred. No. 15;
                                                                                             0
                                                                                             Mismatches
                                                                                          0; Indels
                                                                                                                                                                                                        0 other
                                                                                        0;
                                                                                     Gaps
                                                                                        0;
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26-UIL-2000; 2000US-022054 14-AUG-2000; 200US-022513 14-AUG-2000; 200US-0225214 14-AUG-2000; 200US-022526 14-AUG-2000; 200US-022526 14-AUG-2000; 200US-0225270 14-AUG-2000; 200US-0225270 14-AUG-2000; 200US-0225270 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225275 14-AUG-2000; 200US-0225276 14-AUG-2000; 200US-0225276 14-AUG-2000; 200US-0225276 14-AUG-2000; 200US-0225276 22-AUG-2000; 200US-022666 22-AUG-2000; 200US-0225274 11-SEP-2000; 200US-0229343 11-SEP-2000; 200US-0229343 11-SEP-2000; 200US-0229343 11-SEP-2000; 200US-0229343 11-SEP-2000; 200US-0229343 11-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 10-SEP-2000; 200US-0231444 11-SEP-2000; 200US-0231444	WO200157182-A2. 09-AUG-2001. 17-JAN-2001; 2001WO-US01354. 31-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-0180628. 24-FEB-2000; 2000US-01806350. 16-MAR-2000; 2000US-019874. 17-MAR-2000; 2000US-0198123. 19-MAY-2000; 2000US-0198123. 19-MAY-2000; 2000US-025515. 07-JUN-2000; 2000US-025486. 30-JUN-2000; 2000US-021486. 30-JUN-2000; 2000US-021486. 30-JUN-2000; 2000US-021486. 30-JUN-2000; 2000US-021486. 31-JUL-2000; 2000US-021647. 11-JUL-2000; 2000US-021649. 11-JUL-2000; 2000US-021689. 11-JUL-2000; 2000US-021689. 11-JUL-2000; 2000US-021689.	AAK83089; 07-NOV-2001 (first entry) Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37901. Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds. Homo sapiens.
יים		
08-NOV-2000 017-NOV-2000 117-NOV-2000 01-DEC-2000 05-DEC-2000 05-DEC-2000	29-SEP-200 29-SEP-200 29-SEP-200 29-SEP-200 02-OCT-200 02-OCT-200 02-OCT-200 02-OCT-200 02-OCT-200 02-OCT-200 02-OCT-200 03-OCT-200 03-OCT-200 04-OCT-200 05-OCT-200 06-OCT-200 07-OCT-200 07-OCT-200 08-OCT-200 08-OCT-200 08-OCT-200 08-OCT-200 09-OCT-200	14-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 21-SEP-200 21-SEP-200 25-SEP-200 25-SEP-200 27-SEP-200
2000US - 200	00000000000000000000000000000000000000	00000000000000000000000000000000000000
\$-0246477 \$-0246477 \$-0246524 \$-0246525 \$-0246525 \$-0246527 \$-0246528 \$-0246528 \$-0246610 \$-0249209 \$-0249209 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249211 \$-0249215 \$-0249215 \$-0249215 \$-0249216 \$-0249215 \$-0249216	0236367 0236369 0236369 0236369 0236370 0236370 0237038 0237039 0237039 0237039 0237040 0239937 0241785 0241787 02411808 02411809 02411809	0232400. 0232401. 0233063. 0233064. 0233065. 0234274. 0234274. 0234997. 0234998. 0234998. 0235836.
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RESULT 11
AAK830
ID AAK830
XX
AC AAK830
XX
O7-NOV
XX
UMAN
DE Human
XX
KW Human
XX
Cytost
XX
Cytost
XX
O9-AUG
XX
D9-AUG
XX
PR 31-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) cproteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cthat affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting cc the nucleic acids into a host cell and culturing the cell to express the cc protein. (I) proteins and polynucleotides may be used to provent. Cc diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present human immune/haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK94902 to AAK94903 and AAM82169 cc represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.1%; S
Best Local Similarity 100.0%;
Matches 17; Conservative 0;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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       31-JAN-2000; 2000US-0179065.
                                          17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37902
                                                                                                                                                                                                                                                                                                 07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                           AAK83090;
                                                                                                                                                                                                                                                                                                                                                                              AAK83090 standard; DNA; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 225 BP; 52 A; 55 C;
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                                                                               09-AUG-2001
                                                                                                                     WO200157182-A2
                                                                                                                                                           Homo sapiens.
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2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0254097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 G; 63 T; 0 other;
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    22-AUG-2
23-AUG-2
30-AUG-2
310-AUG-2
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14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
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24-FEB-2000;
  2000US-0233063
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2000US-0229343
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2000US-0229343
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2000US-0229513
2000US-0230437
2000US-0231243
2000US-0231243
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2000US-0231244
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2000US-0186350.
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02-OCT-2000

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09-NOV-2000

09-NOV-2000

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01-DEC-2000

08-DEC-2000

ucleic acids encoding useful for preventing, metastasis -
                                                                                        2001-483426/52.
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-2000;
-2000;
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                                                                                                                                   Barash
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2000US-0246527.
2000US-0246527.
2000US-0246609.
2000US-0246611.
2000US-0249209.
2000US-0249219.
2000US-0249211.
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2000US-0251166.
2000US-02511856.
2000US-02511856.
2000US-0251868.
2000US-02511989.
2000US-0251999.
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2000US-0244617
2000US-0246474
2000US-0246475
2000US-0246476
2000US-0246476
2000US-0246478
2000US-0246523
2000US-0246523
2000US-0246523
                                                                                                                                SC,
                                                                                                                                                                             SCI INC
                    human immune/hematopoietic diagnosing and/or treating
                                                                                                                                MS
                      antigen
cancers
                        polypeptides, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC anks4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CI treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoietic acids considered cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic conservation. Sequences from the present invention. AAK54942 to AAK8450 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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Best Local :
31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

11-MAR-2000

11-MAR-2000

07-JUN-2000

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28-JUN-2000

207-JUL-2000

07-JUL-2000

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26-JUL-2000

26-JUL-2000

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26-JUL-2000

26-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                           02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                         WO200155314-A2
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human digestive system antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK90734 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AAAGAGAGGCTCAGAGA 141
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mes 17; Conserv
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 2000US-0179065
2000US-0186628
2000US-0188664
2000US-0188653
2000US-018974
2000US-0199076
2000US-0199123
2000US-0209467
2000US-021135
2000US-0216880
2000US-02116880
2000US-0217496
2000US-0217487
2000US-0217496
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                               2001WO-US01324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO 37902; 3071pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; Hirschsprung's dis
sorder; Meckel's diverticulum;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  chronic colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 appendicitis;
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Query Match
Best Local S
Matches 17
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                                                                                                                          The present invention provides the protein and coding sequences of number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                              Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \frac{1}{2}
                                                                                           Sequence 225
                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4310; 986pp; English.
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ch 11.1%;
l Similarity 100.0%;
17; Conservative
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2000US-0246525.
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2000US-024921.
2000US-025921.
                                                                                           BP;
                                                                                           52 A;
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Score 17; DB; Pred. No. 49; 0; Mismatches
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                        DB;
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                                       22;
                                                                                              other;
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125 AAAGAGAGGCTCAGAGA 141

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Indels

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את היה לי לי סיסים ים יה יה יה לי היה לי את היה לי היה לי היה לי היה לו הי

14-AUG 2000
11-AUG
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2000US-0234401
2000US-02341785
2000US-02441785
2000US-02441808
2000US-02444785

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RESULT :
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04-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; digestive system antigen; gene therapy; can ulcerative colitis; infection; Hirschsprung's disorderstive system disorder; Meckel's diverticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001;
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2000US-0198123.
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2000US-0205515.
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llum; ds.
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chronic colitis;
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Query Match
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                                                                                                                                                                                                                                                  gene therapy;
                                                                                                                                                                                                                                                                                                              Human secreted protein 5' EST, SEQ ID NO: 9304.
                                                                                                                                                                                                                                                                                                                                                       06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                AAC05229;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC05229 standard; cDNA; 311 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 225 BP; 52 A; 55 C; 55 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human digestive system antiques. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendictis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antiqen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
    (GEST ) GENSET
                                                                                                                             06-SEP-2000
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4312; 986pp; English.
                                             26-FEB-1999;
                                                                                    21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
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7-NOV-2000;
1-DEC-2000;
1-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match 11.1%; Score 17; DB 22; Length 225; Local Similarity 100.0%; Pred. No. 49; Local Similarity 0; Mismatches 0; Indels as 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-502630/55.
                                                                                                                                                                                                                                             5' EST; expressed sequence tag; secreted protein; cDNA isolation;
herapy; chromosome mapping; ss.
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2001US-0259678
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                                           99US-0122487
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Best Local :
                                                                                                                                              12-MAR-1999;
11-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORR has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                    Human: secreted protein; cytostatic; antiarthritic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antiinflammatory; mostropic; neuroprotective; antidiabetic; tranquiliser; vulnerary; antiacterial; antityporiatic; antiarthythmic; antirhematic; cardiant; anti-HIV; autoimmune disorder; allergic condition; cardiovascular disorder; cancer; neurological disease; tissue repair; ss.
WPI; 2000-638176/61
P-PSDB; AAB44853.
                                                                                                                                                                                                                                                                                                            WO200055176-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 311 BP; 90 A; 74 C; 63 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 9304; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                              09-MAR-2000; 2000WO-US06057
                                                                                                                                                                                                                                                                     21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein encoding cDNA for gene 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC79872 standard; cDNA; 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 GAGGCTCAGAGACTTTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 gaggctcagagactttg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-500381/45.
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17; Conserv
                                                              Ruben SM,
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                                                                                                                                         99US-0124142.
99US-0138597.
99US-0168666.
                                                              Komatsoulis
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DB 21; Length 311; 48; 0,

Indels

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Matches

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We would be human secreted proteins useful for diagnosis, prevention and Preatment of disorders including neurological, cell proliferative, Pr cardiovascular, and autoimmune/inflammatory disorders and microbial infections in fections.

XX Claim la; Page 349; 405pp; English.

XX Claim la; Page 349; English.

XX Claim la; Page 349; English.

XX Claim la; Page 349; A
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Query Match Best Local Matches Local Similarity nes 17; Conserv Conservative 11.18; 0, Score 17; Pred. No. Mismatches DB 21; 0; Length 657; Indels 0 Gaps 0;

Search completed: August 3, 2002, 01:50:02 Job time: 32187 sec

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GCTCAGAGACTTTGTGG

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133 GCTCAGAGACTTTGTGG 149

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Minimum DB seq length: 0
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153
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AZ846867	AI638930	CNS02EDQ	BF147109	BG858209	AG131555	AW996787	BE895133	AU125712	BF239967	AW997058	AI890775	AL601246	BB834922	вв830730	BB461065	BB155356	ID		
AZ846867 2M0147B18	AI638930 AEMTAL55	AL193607 Tetraodon	BF147109 uy07a12.y	BG858209 1024056D0	AG131555 Pan trogl	AW996787 QV3-BN004	BE895133 601436060	AU125712 AU125712	BF239967 601905170	AW997058 QV3-BN004	AI890775 wm95fll.x	AL601246 DKFZp313J	BB834922 BB834922	вв830730 вв830730	BB461065 BB461065	вв155356 вв155356	Description		

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11.8	11.8			11.8		11.8	11.8	11.8		11.8	11.8		11.8		11.8		11.8	11.8	٠	11.8			11.8	11.8	11.8	12.4	12.4
1176	993	969	901	810	709	703	700	698	663	655	607	587	545	530	517	507	495	491	481	456	451	448	440	380	329	932	654
10	12	12	10	10	12	12				10	10	12	10	9	12	10	12	10	9	10	9	12	12	9	9	10	9
BG036467	CNS06G3K	AG134136	BE259673	BG666296	AQ545887	AG144450	BG176934	AW639551	AL638257	BJ043477	вл060189	AZ096348	вл068556	BB752282	AQ168710	BG370667	BH570623	вJ029393	AW634969	R40931	AI465697	AQ024759	AQ997521	AA148843	AA856136	BG169355	AI623066
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ALIGNMENTS

RESULT BB155356 LOCUS

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS
Bullianing to Market Alexander Alexander Street Street Street	Mus musculus	house mouse.	EST.	BB155356.2 GI:16268254	BB155356	DNA-binding protein (CHD-1) mRNA, mRNA sequence.	musculus cDNA clone A130024L16 3' similar to L10410 Mouse	BB155356 RIKEN full-length enriched, 16 days neonate thymus Mus	BB155356 619 bp mrNA linear EST 18-OCT-2001

COMMENT

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentla; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 519)

RS Arakawa, T., Carninci, P., Fikuda, S., Firuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Namura, K., Ohno, M., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., Staki, C., Sasaki, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

AL Unpublished (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Dhysical and Chemical Research (BIKEN)

1-7-22 Sushito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura Fax: 81-45-503-9216

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RESULT
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         BB461065 660 bp mRNA linear EST 25-OCT-2001 BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
BB461065
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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/dev_stage="16 days neonate"
/lab_host="DH10B"
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug,Y. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Arakawa, T., Carninci, P., Fukuda, S.,
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Please visit our web site (http://genome.gsc.riken.go.jp/)
further details.
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                                   contributed to prepare mouse tissues. 1st strand
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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/clone="D130070B13"
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Akinura, T. Arakawa, T. Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishi, Y., Ito, M., Kawai, J., Konjima, Y., Konno, H., Koda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Saito, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Saito, R., Shinagawa, A., Shiraki, T., Togabe, Y., Saito, R., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., et al. 201)
                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Tex: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB830730 RIKEN full-length enriched, mammary gland RCB-0527
JYG-MC(B) CDNA Mus muscullus CDNA clone G930013K04 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Yoshihide Hayashizaki
                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Su,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
BB830730
BB830730.1 GI:17008973
Computer-based methods for the mouse full-length cDNA
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BB834922 RIKEN
Jyg-MC(B) cDNA I
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RESULT BB830730

DEFINITION

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562

BASE COUNT ORIGIN

211

Matches

102;

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

COMMENT

JOURNAL

TITLE

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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p. Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
waqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
waqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
,S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Ress. 10 (11), 1757-1771 (2000)
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EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chord
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1 (bases 1 to 446)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                      Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL601246
430 bp mRNA linear EST 14-AUG DKFZp313J1040_rl 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313J1040 5', mRNA sequence.
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e mouse tissues.
                                                                                                                                                                                                                                                       This clone (DKFZp313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubherweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                       No s1 sequence available
                                                                                                                                                                                                                                                                                                                                           German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiemann, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bloecker, H., Boecher, M., Brandt, P.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Y. and Hayashizaki, Y
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                   /note="Vector: pTriplEx2; Site_1:
cDNA-collection"
a 81 c 86 g 100 t
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/clone="g930033J21"
/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
99 c 108 g 100 t
                                                                                                     /clone="DKFZp313J1040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
                                                                               /lab_host="DH10B"
                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                 ocation/Qualifiers
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Pred. No.
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                                                         SfiIA; Site_2:
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                                                                                                                                                      76 CAGACCCGTGCAGACTACCTCATCAAA 102
                                                                                                                                                                                                        Local
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                                                                                                                      CAGACCCGTGCAGACTACCTCATCAAA 307
AW997058 686 bp mrNA lir
QV3-BN0047-150400-152-c03 BN0047 Homo sapiens
AW997058
                                                                                                                                                                                        l Similarity 100.
27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1924 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI890775.1
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                                                                                                                                                                                                                                                                                                          /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2443725"

/clone_lib="NCI_CGAP_Ut2"

/tissue_type="moderately-differentiated

/denocarcinoma, 3 pooled tumors"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                 cDNA,
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               mRNA sequence.
                                   EST 05-JUN-2000
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AW997058.1 GI:8257292

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 821)
1 (Dases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Coldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                            BF239967 821 bp mRNA linear EST 14-NG 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 19
High quality sequence stop: 678.
Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150
400-152-c038t3-2000-04-154t4-1)
seq primer: puc 18 forward
useq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

154 c 126 g 241 t
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/dev_stage="Adult"
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                                                                                                                                  Contact: Takao Isógai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai.T.
Isogai.T.
HRI human cDNA project (Ota.T., Wakamatsu,A., Ozawa,M., Ishii,S. Saito,K., Yamamoto.J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzu,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM1033 row: K. COLumn: 18
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Contact: Robert Strausberg, Ph.D.
Email: genomics&lri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 866) Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU125712 NT2RM4 Homo sapiens cDNA clone NT2RM4002061 5', mRNA
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Tissue Procurement: ATCC
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/Clone=1hb="NH_MGC_54"
/tissue_type="from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="philoB (T1 phage-resistant)"
/lab_host="philoB (T2 phage-resistant)"
/lab_host="philoB (T2 phage-resistant)"
/lab_host="philoB (T1 p
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/db_xref="taxon:9606"
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 CAGACCCGTGCAGACTACCTCATCAAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGACCCGTGCAGACTACCTCATCAAA 521
                                  27;
                                                                                                                                                                                                                                                                                                                 Plate: LLAM9753 row: h column: High quality sequence stop: 488.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence
BE895133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE895133 1028 bp m 601436060F1 NIH_MGC_72 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image_llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                         /lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."

1 205 c 238 g 198 t
                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
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/cell_line="NT2"
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/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
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19 GATAAAAAACCACAAGCAAAACAGTT 44
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AG131555 1200
Pan troglodytes DNA, clone:
AG131555
AG131555.1 GI:16661233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
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QV3-BN0047-230200-102-d03 BN0047
AM996787
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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High quality sequence stop: 337,
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                    note-"Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0047"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                             17.0%;
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sapiens cDNA,
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                                                                   linear
                                              survey
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RESULT 13
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 1312)

Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Sliflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000

Duke University
Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
23; Conserv
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii. Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                   BG858209
BG858209.1 GI:14239393
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG858209 1312 bp mRNA linear EST 29-MAY-: 1024056D08.xl C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
PAN Library clone:PTB-143K14.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1200)
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R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing: -21M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-143K14.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
371 c 199 g 39 t 65 others
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100.0%; Pre
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ORGANISM
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Best Local
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                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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22; Conserv
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Fax: 919 613 8177
Email: chauser@dul
                                                                                                                                                                                                            Email: mouseesf@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Profest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                        MGI:1419614
Seq primer: Primer name ambiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 217)
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:: 314 286 1810
                                                                                                                                   quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mid-log phase in TAP (acetate containing) medium in the light. TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. POLYA MRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the BCORI (5') and XhOI (3') sites. Paluescript II (SK plasmids were excised from the lambda ZAP clones by superinfection with Exasist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript II SK.; Site_1: EcoRT; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="texon:3055"
      /strain="CD-1"
/db_xref="taxon:10090"
                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Gaps

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Murinae; Mus

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Best Local
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Submitted (12-APR 2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovi genome. For more information, please take a look at http://www.genoscope.ons.fr/Tetraodon.
                                                                                                                                                                                                                                                                                          2 (bases 1 to 404)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 404)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
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19; Conserv
                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                           Genoscope
                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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AL193607.1 GI:7831713
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/note="Organ: testis; Vector: pBluescript SK+ (Stratagene ); Site_1: XhoI; Site_2: EBORI; cDNA oligo dT-primed |
| 5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTTTT-3' | and directionally |
| cloned using 5' linkers 5'-AATTCGCACGAG3' and |
| 5'-CTCGTGCCGC3'. Size selection of >400bb material gives average insert size ranging from 1-2 kb. Library was mass excised (from lambda-UnizAP-XR) and resulting from 1-2 kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Health Sciences). Original lambda-based library is available through ATCC, catalog \#63422." a 38 c 60 g 73 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single-stranded phagemids were prepped and tranformed into DH10B. Library contains 98% recombinants. References: J. Androl. 20:635-639 and Gene 25:263-269. Library constructed and donated by J. McCarrey, Ph.D. (Southwest roundation for Blomedical Research, Dept. of Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:3657310"
/clone_lib_"McCarrey Eddy spermatocytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="spermatocytes, pooled from multiple mice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%;
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Pred. No.
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                                                                                     part of a large nigroviridis
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RESULT 1
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Matches

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SOURCE KEYWORDS

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Search completed: August 2, Job time: 30148 sec
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Best Local Similarity
Matches 19; Conserv
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                                                                                                             Conservative
                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db.xref="taxon:99883"
/clone="262M09"
/clone_11b="G"
/clone_11b="G"
/note="Genoscope sequence ID : COAG2
PUC-Ori"
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25
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                                                                                                                                  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match Length DB
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Sequence 3 from Patent W09639505.
A58684
A58684.1 GI:3714247
                                                                                                         Patent: WO 9639505-A 3 12-DEC-1996;
ISIS INVOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
                                                                                                                                                                                                                           unclassified.

1 (bases 1 to 153)

Griffiths, R. and Tiwari, B.

AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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                                                                                                                            AF004397 6872 bp mRNA Gallus gallus chromo-helicase-DNA-binding protein, variant with hydrophilic domain,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
A58691
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                         Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 9639505-A 10 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
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on the Z chromosome
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51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAA 110

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Query Match Best Local Similarity

Matches

103;

Conservative

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Score 103; Pred. No. Mismatches

DB 5; 5.2e-49;

Length Indels

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Submitted (16-MAY-1997) Zoology,
Glasgow G12 8Q0, UK
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Gene 197 (1-2), 225-229 (1997)
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CKVLKORPREYALKKOPSYIGGHESLELRDYOLNGLWILAHSWCKGNSCTLADERGLG
CKVLKORPREYALKKOPSYIGGHESLELRDYOLNGLWILAHSWCKGNSCTLADERGLG
KTIQTISELAVLFHEHOLYGPELLRVDLSTLTSWORELOTWAPOWNAVVYLGDITSRN
MIRTHEWMHPQTKRLKRNILLTTYEILLKDKSFLGGLWAPFIGVDEAHRLKNDDSLLY
RTLLDEKSNHRLLITGTPLONSLKELMSLLHFIMPEKFSSWEDDFEEHGKGREYGYAS
LHKELEPFLLRRVKKOYEKSLPAKVEGULREMSKALOKOYYKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCNHCYLLKPDONEFYNKOEALOHLIRSGKLILLDKLLIRLR
ERGNRYLIFSOMVRMLDILABYLKYROPPFORLDGSIKGELRKOALDHENAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWHPQNDLOAQARAHRIGGKKQVNIYRLVTKGS
VEEDILERAKKMVLDHLYQRHDTTGKTVLHTGSTPSSSTPFNKEELSAILKFGAEE
LFKEPEGEEDGEPOEMDIDEILKRAETRENEPGPLTVODELLSOPKVANFSNMDEDDIE
LEPERNSRNWEEIIPESORRRIEEEEROKELEEIYMLPRMRNCAKQISFRSGSGRRSR
SRRYSGSDSDSTTERKEPKKRGRPRTIFRENIKGFSDAEIRREIXSGVKANFSNMDEDDIE
SRRYSGSDSDSTTERKEPKKRGRPRTIFRENIKGFSDAEIRREIXSGVGVNAKVGPTFRISGV
QVNAKLVISHEEELAPLHKSIPSDPEEKKRYVIPCHTKAAHFDIDMGKEDDSNLLVGI
YEYGYGSWEMIKMDPDLSLTQKILPDDDKKPOAKQLOTRADYLIKLLNKDLARKEAQ
RLAGAGNSKRKTRNKKNKKASKIKEEIKSDSSPQFSEKSDEDDEEEDNKDEIVSVK
RHAGAGNSKRKTRNKKNKKKSKIKEEIKSDSSPQFSEKSDEDDEEEDNKDEITYSVK
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DSESAEDGDKSSCEESEDYEPKNKYKSRKPPSTIKPKSGKKFQGKKRQLDSSEEEE
DDDEDYDKRGGRRQATVWSYKEAEFTWTDSDDLLEVGGEDVPQTEEDEFETIEKFMD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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                                       HRSPFEHSSDHKSTPEHTWSSRKT"
4341. .4604
                                                                                                        THY I RNPDYERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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228. .5654
/gene="CHD-Z"
                                                                                                                                                                                                                 KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
                                                                                                                                                                                                                                                         ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
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/db_xref="GI:2501846"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain
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                                                                                                             1960 GAAG 1963
                                                                                                                                                                           130 GAAG 133
                                                                                                                                                                                                                                                                                                                                                                                         tch 41.8%; Score 64; DB 5; L
al Similarity 100.0%; Pred. No. 3.1e-26;
64; Conservative 0; Mismatches 0;
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Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging and Cancer, Tohoku Univ.: 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (Tel:022-272-9499, Fax:022-272-3982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Arrhosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (library: lambda gtll) 13 day embryo lens cDNA to mRNA, clone JF11.
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//db_xref=**G1:391640**
//db_xref=**G1:391640**
//translation-**melkKCCNHCYLIKPPDDNEFYNKQEALQHLIRSSGKLILLOKL
//translation-**MelkKCCNHCYLIKPPDDNEFYNKQEALQHLIRSSGKLILLOKL
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//translation-**MelkKCNTLDHLVIQRHDTTOKTVLHTGSTPSSSTPFNKEELSALLK
//translation-**MelkKCNTLDHLVIQRHDTTOKTVLHTGSTPSSSTPFNKEELSALLK
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/clone_lib="lambda gtl1"
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91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACA 137
                                                                                                                                                         91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACA 137
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nes 47; Conserv
                                                                                                                                                                                     Match 30.7%; Score 47; DB 6; Local Similarity 100.0%; Pred. No. 2.6e-16; es 47; Conservative 0; Mismatches 0;
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153 bp
Sequence 5 from Patent W09639505.
A58686
A58686.1 GI:3714249
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Sequence 15 from Patent WO9639505.
A58696
                                                                                                                                                                                                                                                                                                                                                   Other publication AU 5906996 961224.
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Griffiths, R. and Ti
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Sequence 4 from Patent W09639505,
A58685
                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 9639505-A 15 12-DEC-1996;
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Griffiths, R. and Tiw
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Griffiths,R. and Ti
AVIAN GHD GENES AND
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Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and sNF2/SWIZ-like helicase domain SNF2/SWIZ-like helicase domain SNF2/SWIZ-like helicase domain proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
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IAHSNQKSAAGLEDYYCKWQGLEYSECSWEDGALISKKRGTCIDEYSENQKSTPFK
DCKVLKQRFREYVALKKOPSYIGGHEGLELDYDCLIWLAHSWCKGNSCILADEWL
CKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVYYLGDINSR
MNIRTHEWMHPQTKRLKFNILLTTYEILLKDKAFLGGLIWAFIQVDEAHRLKNDDSLL
YKTLIDFKSNHRFLLTGTPLQNSLKELWSLHFIMPEKFSWEDFEEEHKGREYGYA
SIHKELEPFLLRVKKOVEKSLPAKVEQILRHEMSALQKQYYKWILTRWYKALSKGSK
SGTSGFLNIMMETKKCONHCYLIKPDNNEFYNKQEALQHLHESGKLILTRUK
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RQPQQAQQQRPASSNSGSEEDSSSSEDDSSSGAKRKKHDEDBWQMSGSGSESQLE
SDSESEERDKSSCDTESDY EPKNKVRSRKPQNRSKSKGKKILGQXKRQIDSSEDE
DEDYINDKRSSCRGAETVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEDEEFETIERVM
DCRYGRKGATGATTTIYAVEADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
                                     RERGNRVLIFSQMVRMLDILAEYLKYROFPFORLDGSIKGELRKOALDHFNAEGSEDF
CFILSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGOKKOVNIYRLVTKG
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ELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNMDEDDI
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/translation="MNGHSDEESVRNGSGESSQSGDDCGSASGSGSGSSSGSSSDGSS
                                                                                                                                                                                                                                                                                                                                                                                                            /product="DNA-binding protein"
/protein_id="AAB08486.1"
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/db_xref⇔"taxon:10090"
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Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Genome Research Institute, National Institutes of Health, 49 Convent Drive, Bethesda, MD 20892-4442, USA Location/Qualifiers
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1 (bases 1 to 5947),

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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25; Conservative
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                             /Godon_start=1
//product="CHD1"
/product="CHD1"
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RSRRYSGSDSDSISEKRPKKRGRPRI I PRENI KGFSDAEI RRFIK SYKKEGEDELERL
DA IARDAEL/UNKSET DLERLGELVIINGCYWALKDSSSGTBRAGGRLGKVKGFPERI SG
VOVNAKLVI AHEDELI FLHKSI PSDPERKOYT I PCHTKAHFDI DMCKEDDSNILI G
I YEKGYGSWEMI KIMDPDLSI THIK ILDDDDKKEDAKOLOJTRADVILIKLISRDIAKREA
ORLCGAGGSKRRKTRAKKSKAMKSI KVKEEI KSDSSPLPSEKSDEDDDKLINDSKPESK
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QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHEWDHYRQDSRYYSDREKHRKLDD
HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
HRARASGGPRSPLDQRSPYGSRSPFEHSABHRSTPEHTWSSRKT"

a 1067 c 1319 g 1224 t
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GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
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164. .5293
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1. .5947
{	t SRNMIRTHEWTHQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDS}
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/db_xref="taxon:9606"
/chromosome="5"
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MEDLINE REFERENCE

JOURNAL

FEATURES

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gene CDS

LLYKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYG

REFERENCE AUTHORS TITLE

RESULT 11 AF006513

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ORIGIN BASE COUNT

Query Match Best Local :

Matches

VERSION KEYWORDS

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AC092372/c
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
AC092372.3 GI:17402768
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced 91:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
WWW.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-0UL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                               Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                   2: This insert is not the entire sequence of the clone (entire
sence is 146.7kb). It is clipped at the overlap with ACO12624.
number of bases overlapped is 90404.
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RLDAIARDAELVUKSETDLERLGELVHNGCIKALKDSSGGTERTGGRLGKVKROGPTERI
SCYQVNAKLVILSHEEELIPLHKSIFSDEERKROYTISCHFYKAHEDLOMGKEDDSNLL
IGIYEYGYGSWEMIKMDPLSLTHKILPDDDDKKPQAKOLOTRADYLIKLSRDLAKK
EALSGAGSSKRRKARAKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
ERGKKSSYSDAPVHITASGEPVPISEESSELDOKTFSICKRRMRVKANLKQLDFPEK
GLSEREGLEHTPQCLIKIGHITECLKRYTNPEQIKOWRKNLMIFVSKFTEFDARKLH
KLYKHAIKKROESQONSONSNUKNHPUTRNDPVERLKEWINHDDSSRDSYSSDPHJTO
YHDHHKDRHQGDSYKKSDSRKFPYSSFSNGKDHRDMDHYKODSRYYSDREKHRKLDDH
RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHKSSRDYRYHSDWOMDH
RASSGCFRSPLDQRSYGSRSPEBISVEHKSTPEHTMSSRKT"
30 a 1004 c 1243 g 1570 t
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SKGSTSGFINIMELKKCCHICYLIKPDNINEFYINGEALQHLIRSSGKLIILDKILI
RLREBGNEVLIFEQAWFMLDILARFIKYRQFPEPRILDGSIKGELRKQALDHFNAEGSE
DFCFILISTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVT
KGSVEEDILERAKKMVLDHLVIQRMDTTGKTVLHTGSAPSSSTPFNKEELSAILKFG
AEELFKEPEGEBOEDQENDIDILIKRATHHNEPGPLTVGDELLSQBKVANFSNMDED
DIELEPERNSKNWEEIIPEDQRRRLEEEERQKELEEIYMLPRMRNCAKQISFNGSEGR
/clone="RP11-58M12"
18862 c 17827 g 30409 t
                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USJ
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUN-2001)
Drive, Walnut Creek, CA
4 (bases 1 to 134365)
   Homo sapiens
Eukaryota; M
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AC021449.3 GI:10047806
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DOE Joint Genome Institute and
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AC012624
AC012624.6 GI:14993679
                                                 HTG; HTGS_PHASE1;
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/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                      /clone="CTD-2082I17"
24497 c 25503 g 43951 t
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                      .134365
                                                                                                                                                                                                                                                           15.0%; Scc
100.0%; Pr
.... 0;
                                                                                                         143079 bp DNA clone RP11-58M12, WORKING
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100.0%;
                                                 HTGS_DRAFT.
                                                                                                                                                                                                                                                                              Score 23;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                  Mismatches
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. 0.021;
                                                                                                                                                                                                                                                                             DB 9; Length 134365; 0.021;
                                                                                                            DRAFT
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                                                                                                          linear HT SEQUENCE,
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REFERENCE
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TITLE
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo, sapiens, clone RP11-58M12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144700; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Center clone name: 58_M_12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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46906 47005: gap of 100 bp 14825 bp in length 51831 51930: contig of 4825 bp in length 51831 51930: gap of 100 bp 100 51931 62619: contig of 10689 bp in length 62620 62719: gap of 100 bp 100 51930 bp in length 75409 75508: gap of 100 bp 100 519508: gap of 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38820: contig of 38820 bp in length

38821 38920: gap of 100 bp

38921 40411: contig of 1491 bp in length

40412 40511: gap of 100 bp

40512 43279: contig of 2768 bp in length

43380 43379: gap of 100 bp

43380 43379: contig of 3526 bp in length
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COMMENT

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JOURNAL
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AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
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AC008531
                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
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                                                                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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Best Local
                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 CAGACCCGTGCAGACTACCTCAT 98
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                     Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AC008531 145659 bp DNA linear HTG 14-FEB-2001
Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14559)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 15.0%; Score 23; DB 2; Le Similarity 100.0%; Pred. No. 0.021; 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 AC008531.3 GI:12830078
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                2 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                          sequencing of Human Chromosome 5
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92617 106409: contig of 13793 bp in length
106401 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length.
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a 26246 c 26678 g 45278 t
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106510. .143079
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92617. .106409
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62720. .75408
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51931. .62619
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38921. .40411
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clone_end:SP6
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43380. 46905
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47006. .51830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
40512. .43279
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/clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
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ORIGIN
Db 46815 CAGACCCGTGCAGACTACCTCAT 46837
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                                                                                                                                     Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                  76 CAGACCCGTGCAGACTACCTCAT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.
*NOTE: This is a 'working draft' sequence. It currently
*consists of 7 contigs. Gaps between the contigs
*are represented as runs of N. The order of the pieces
*is believed to be correct as given, however the sizes
*of the gaps between them are based on estimates that have
*provided by the submittor.

*This sequence will be replaced
*by the finished sequence as soon as it is available and
*the accession number will be preserved.

56174 contig of 56174 bp in length
*100975 113127 contig of 44600 bp in length
*11328 118190 contig of 44600 bp in length
*11328 118291 gap of unknown length
*11328 118291 gap of unknown length
*11891 11894 contig of 4063 bp in length
*11891 11895 12397; contig of 1404 bp in length
*113298 13397; contig of 1404 bp in length
*113298 13397; contig of 3503 bp in length
*113298 13397; contig of 5507 bp in length
*113298 13397; contig of 1404 bp in length
*113298 13397; contig of 1507 bp in length
*113298 13597; contig of 2262 bp in length
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Center Project Name: 369535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
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                                                                                                                                                                                                                                                                                                                                            42561 a
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                 /clone_lib="CalTech human BAC library C"
26309 c 27580 g 48609 t 600 others
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="CTC-480B11"
                                                                                                                                 15.0%; Score 23;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Qualifiers
                                                                                                                                     Mismatches
                                                                                                                                                                DB 2; Length 145659;
0.021;
                                                                                                                                     0; Indels
                                                                                                                                     0; Gaps
                                                                                                                                     0,
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Search completed: August 3, 2002, 01:42:44 Job time: 40734 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                  O
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                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                            Score
            153
103
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153
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                           Length
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Chicken CHD-1A gen
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Chicken CHD-W gene
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-NUL-90	05 - JUN-	12-DEC-	WO963	Key misc_	Gallus	Bird; CHD-1	Chick	12-MA	AAT42757	JLT 1 12757 AAT427		45	43	42 42	40	3 3 8 9 8	37	3 5 5	ω (1 4)	ω ω 2 ω	31	30	28	26	25	23 24	22	20	19 19	17	15 16	14	12
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				lifiers s 52-81 are a are ignored in sequence give		determination; chromodomain-Helicase-DNA binding ${\rm ID\text{-}W};~W$ chromosome; ss.				BP.	ALIGNMENTS	AAF67429	AAQ45230	AAA42896	AAC15424	AAF84535 ABA95621	AAZ60239	AAF84524 AAF8453:2	AAF84525	AAF84527	AAF84531	AAF84529	AAF84530	ABA17489 AAT81515	AAI63751	AAK53038 AAT99401	AAK52054	AAC49707	AAK88882	AAZ65937	AAZ01079 AAZ01156	AAZ01319	AAV20467
				repeat of bases 22-51 1 the translated amino 2n in Fig 3"		-DNA binding 1;						Novel	Partial	Human secre	Human	Trunca Wheat	Wheat	Wheat Wheat	Wheat	Wheat	Wheat	Wheat		Human Human		Human	Human	Arabid	Human Human		Probe	PCR primer	Human c-myb oncog
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Best Local
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birds
Avian chromodomain-helicase-DNA binding genes determine sex in
                                                       WPI; 1997-043127/04.
                                                                                                       Griffiths R,
                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                              05-JUN-1996;
                                                                                                                                                                                                                                                                                                                 12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken CHD-1A gene
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                                                                                                                                                         (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex determination; chromodomain-Helicase-DNA binding 1 Avian;
chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromodomain-helicase-DNA binding genes determine sex
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                                                                                                       Tiwari B;
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                                                                                                                                                                                                                                                              96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
228..5390
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 153; DB 18;
. No. 4.6e-70;
smatches 0;
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RESULT
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Best Local
                                                                                                                                        WPI; 199
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4160 taaagaccttgcaagaaaggaagcacaaaggcttgctggtgca 4202
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  Claim
                                                        Avian chromodomain-helicase-DNA binding birds - used for sex determn, and to cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding CHD-lA; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chick CHD-W gene fragment.
                                                                                                                                                                                                                        Griffiths R,
                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42758 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 5; 76pp; English
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                                                                                                                                                                                                                                                                              (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAA 110
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                                                                                                                                        1997-043127/04.
DB; AAW08148.
8; Fig 3; 76pp; English
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                                                   for sex determn.
                                                                                                                                                                                                                                                                              INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
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Pred. No.
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                                                        control
                                                                                  genes determine sex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6608;
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Query Match
Best Local
           Matches 47;
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                                                                                                                                                                                                                                                                                                                                                                                        The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe The CHD-W and CHD-1A give located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a training the control of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in Maral 146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, for the characteristic transfer of the charac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                 Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foetus etc. and to manipulate the sex of progeny.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 tacctcattaaattactgaataaagaccttgcaagaaaggaagcaca 137
                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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47; Conservative
30.7%;
ilarity 100.0%;
Conservative
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100.0%; Pred. No.
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Pred. No.
                                                                 DB 18;
. 7.3e-15
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7.3e-15;
es 0;
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                                                                                               Length 1316;
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RESULT
AAT42756
ID AAT4

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AAT42756 standard; DNA; 153

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91

91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128

tacctcattaaattactgaataaagaccttgcaagaaa 128

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RESULT
AAT42759
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   Matches
                Query Match
Best Local :
                                                                                             Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1a (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-IA (see also AAT42751) and GHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                            Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                      Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                      Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parus major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Great tit CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT42759 standard; DNA;
                                                                                                                                                                                                                                                                                                 P-PSDB; AAW08149
                                                                                                                                                                                                                                                                                                              WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAAGCACA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex determination; chromodomain-Helicase-DNA binding
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHD-W; W chromosome; ss
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
             24.8%; Score 38; DB 18; 100.0%; Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΒP
                           Length 153;
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AAT42756;

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                                                                                                                                                                                                                                                                              Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                  Avian
birds
                                                              14-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths R,
                                       Altered telomere repeat binding factor 1 gene.
                                                                                  AAV59280;
                                                                                                      AAV59280
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9639505-A1
                                                                                                                                                         74
                                                                                                                                                                              74 TACAGACCCGTGCAGACTACCTCAT 98
                                                                                                                           7
                    human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                         tacagacccgtgcagactacctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                               chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex determination; chromodomain-Helicase-DNA binding
CHD-W; W chromosome; ss.
                                                                                                                                                                    8; Fig 3; 76pp; English.
                                                                                                                                                                                                  25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW08146
                                                                                                                                                                                                                                                      153
                                                                                                      standard;
          ageing; ataxia telangeictasia;
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                    ВP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 52..81
                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                      CDNA;
                                                                                                                                                                                                                                                    Α,
                                                            entry)
                                                                                                                                                                                                           16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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                                                                                                                                                                                                          Score :
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         Down's syndrome; tumour; viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequent translations of the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1280 tacagacccgtgcagactacctcat 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, heteror-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-1998;
13-FEB-1997;
                                                                                Homo sapiens
                                                                                                                                                                                                                  tissue
                                                                                                                                                                                                                                                          vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The altered vertebrate telomere repeat binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide
                                                                                                                                                                                                         cytokine; cell proliferation; cell differentiation; e; peptide therapy; stem cell growth factor; haematog growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                     disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0018628
97US-0800264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
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                                                                                                                                                                     arthritis;
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Pred. No.
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                                                                                                                                                                          inflammation; ss
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0.0021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1311;
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30-JUN-1999;
15-OCT-1999;
17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypopulations and polypopulations are useful in gene therapy, vaccines or peptide therapy. The polypopulates have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 401 BP; 113 A; 87 C; 108 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 628; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT,
                                                                                                                                                                                         Human; lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                        AAF68219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001.
                                                              30-JUN-2000; 2000WO-US18061.
                                                                                                                             WO200100828-A2.
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                        Human lung tumour protein related nucleotide sequence SEQ ID NO:137.
                                                                                                                                                                                                                                                                                          12-APR-2001
                                                                                                                                                                                                                                                                                                                                                       AAF68219 standard; cDNA; 552 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AA000637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                      304 CAGACAAGAAACCCCAGG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 CAGACAAGAAACCCCAGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                        (first entry)
99US-0346492.
99US-0419356.
99US-0466867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 401; 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC triat affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I), Additionally, the
CC NAS may be used to produce the lung-tumour associated protein, according
CC molecules may be used to produce the lung-tumour associated protein. According
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC AAB76848 to AAB76878 represent human lung tumour protein examplification
CC of the present invention.

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                                                                                                                                                                                                                                                                                                             RESULT 10
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Best Local :
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06-MAR-2000;
22-MAR-2000;
10-APR-2000;
27-APR-2000;
                                                                 Transmembrane domain; human; nutrition; cytokine; cell proliferation; differentiation; immune system; stimulator; suppressor; regulator; heamatopoiesis; activin; inhibitor; chemotactic; chemotactic; receptor; haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds.
                                Homo sapiens
                                                                                                                                                            Human lymphoma cell line U937 clone HP10136 cDNA #1.
                                                                                                                                                                                                 21-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                           AAV49574 standard; cDNA to mRNA; 1409 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 552 BP; 220 A; 118 C; 69 G; 144 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 193; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retter MW,
                                                                                                                                                                                                                                      AAV49574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
18; Conserv
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W, Mannion J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; 99US-0476300.
); 2000US-0519642.
); 2000US-0533077.
); 2000US-0546259.
); 2000US-0560406.
); 2000US-0589184.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; 5
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 22; Length 552; Pred. No. 9;
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Location/Qualifiers

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Best Local
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       Wang
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                                                                          06-MAY-1999
                                                                                                                           diagnosis; ss
                                                                                                                                  autoimmune disease;
                                                                                                                                            Human; vesicle trafficking
                                                                                                                                                                                                                                                                                                                                                                     AAV49550-V49599 are cDNA sequences which encode human proteins containing a transmembrane domain. These proteins can be used for, e.g. research and nutrition, and may have cytokine and cell proliferation/differentiation, immune stimulating/suppressing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1997;
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                       (UYSH-) UNIV SHANGHAI SECOND MEDICAL
                                        29-OCT-1997;
                                                         29-OCT-1997;
                                                                                          W09921988-A1
                                                                                                         Homo sapiens
                                                                                                                                                           Human CBFBBA01
                                                                                                                                                                            16-JUL-1999
                                                                                                                                                                                            AAX56240;
                                                                                                                                                                                                             AAX56240 standard;
                                                                                                                                                                                                                                                                                                                                Sequence 1409 BP;
                                                                                                                                                                                                                                                                                                                                                       haematopolesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, re
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                anti-inflammatory or tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9821328-A2
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                                                                                                                                                                                                                                                       taaagaccttgcaagaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein having transmembrane
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SAGAMI CHEM RI
                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Page 153-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                  and nutrition
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEM
                                                                                                                                                           vesicle trafficking protein SEC22b gene
                                        97WO-CN00115
                                                         97WO-CN00115
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                377 A;
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100.0%; Pr
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                                                                                                                                  protein; SEC22b;
es mellitus; mult;
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Pred.
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                                                                                                                                                                                                                                                                                                                                325 G;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamaguchi
                                                                                                                                                                                                                                                                                               . 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                  multiple sclerosis;
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9.
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                                                                                                                                            CBFBBA01;
                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
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                                                                                                                                                                                                                                                                                                      Length 1409;
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                                                                                                                                           cancer;
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RESULT 1
AAV20467/
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Best Local :
The present sequence represents an oncogene from the present invention The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-abl, bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against CBFBBA01 are useful as research reagents, for screening assays and in diagnostic assays, especially for cancer, autoimmune disease, diabetes mellitus and multiple sclerosis. Antagonists and agonists of CBFBBA01 can be used to inhibit or enhance, respectively, the activity of CBFBBA01 or expression of (I). Anti-CBFBBA01 antibodies and CBFBBA01 or its fragments can be used in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endoplasmic reticulum and golgi membranes. CBFBBA01 polynucleotide (I vectors containing (I) and recombinant host cells are useful for recombinant production of CBFBBA01. Both (I), CBFBBA01 and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes CBFBBA01, which is a protein homologous to murine vesicle trafficking protein sec22b. CBFBBA01 is a cytoplasmically orientated integral membrane protein, located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-312961/26.
P-PSDB; AAY09512.
                                                                                              Claim
                                                                                                                        Anticancer composition comprising two anti-sense oligo:nucleotide(s) - targetting cytoplasmic and nuclear oncogene(s)
                                                                                                                                                                   WPI; 1998-229882/20
                                                                                                                                                                                                                                                   15-SEP-1994;
                                                                                                                                                                                                                                                                             15-SEP-1994;
                                                                                                                                                                                                                                                                                                        31-MAR-1998
                                                                                                                                                                                                                                                                                                                                  US5734039-A
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human c-myb oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV20467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1462 BP; 419 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes
                                                                                                                                                                                                                      (UYJE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 TAAAGACCTTGCAAGAAA 128
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     oncogene;
                                                                                                                                                                                                                                                                                                                                                                                        antisense
                                                                                               Column 131-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein useful in treating cancer, autoimmune disease, mellitus and multiple sclerosis
                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                        JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                   94US-0306691
                                                                                                                                                                                                                                                                             94US-0306691
                                                                                                                                                                                                                                                                                                                                                                                       proto-oncogene; neoplastic disease; anticancer;
oligonucleotide; c-myb; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29pp;
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                                                                                              92pp;
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Pred. No.
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                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 T;
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                                                                      invention.
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RESULT 13
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLI/MTGB, E2A/PpI and ALL-1/AF4. The composition is used for treating cance The combination of antisense oligonucleotides has synergistically
                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL)6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7377-BBB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2662 ATTAAATTACTGAATAAA 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL15492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3225 BP; 975 A; 687 C; 698 G; 865 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enhanced ability to inhibit growth of cancer cells.
                                                                             Sequence 59967 BP; 17305 A; 12463 C; 12291 G; 17908 T; 0 other;
                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 40958; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 40958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
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                   Local
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                                                                                                                                                                                                                                                                                                                                   solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
     18;
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AAZ01079

15

AAZ01079 standard; DNA; 47 BP

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RESULT 14
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                                                                                                                                                                   The invention relates to a mammalian PG1 gene and protein, and a set of PG1 bialielic markers. The PG1 polynucleortide and bialielic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PG1 related bialielic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Barly-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PG1 gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
                                                                                                                                          Sequence 19 BP; 9 A; 6 C; 3 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 368; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a prostate cancer associated gene and biallelic markers derived from it
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22-DEC-1997;
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3 aaagcagctacagacca 19
                                                                            Local
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                                                             Conservative
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97US-0996306
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Search completed: August
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                                                                                                                             Query Match
Best Local S
Matches 17
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22-DEC-1997;
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Homo sapiens
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17; Conserv
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Maximum DB seq length: 200000000
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Match Length DB
13736207 segs, 6748477542 residues
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153
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294.307 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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BB461065 BB461065
AL601246 DKFZP311J
BB830730 BB830730
BB831492 BB834923 BB834923 BB83492 BB834924 BB34924
AI89075 wm95f11.x
AW997058 OJ905170
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AZ570983 281PvC04
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AA234796	AA955076	AA267899	AQ816352	BB810785	AI902726	BB137014	BF289372	AA937817	AA354813	BB137675	BB560958	BB402744	BB031183	BB030255	BE768484	AV222464	BB164147	AV375787	AV312872	AV317684	AV317344	E842	84	Ν	AZ200903	Ħ	AZ963945	
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ALIGNMENTS

REFERENCE AUTHORS RESULT BB155356 LOCUS KEYWORDS SOURCE ACCESSION VERSION COMMENT DEFINITION ORGANISM Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1330 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
On Jun 29, 2000 this sequence version replaced gi:8811286.
On Jun 29, 2000 this sequence version replaced gi:8811286.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yoskohama Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 7el: 81-45-503-9216
Fax: 81-45-503-9216 Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)

1 (bases 1 to 619)

Arakawa, T., Carninci, P., Fukuda, S., Teruno, M., Hanagaki, T., Hara, A. Arakawa, T., Carninci, P., Fukuda, S., Teruno, M., Hanagaki, T., Mono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shirakki, T., Soyabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Havashizaki, Y., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., And Havashizaki, Y. BB155356
619 bp mRNA linear EST 18-OCT-:
BB155356 RIKEN full-length enriched, 16 days neonate thymus Mus
musculus cDNA clone Al30024L16 3' similar to L10410 Mouse
DNA-binding protein (CHD-1) mRNA, mRNA sequence.
BB155356 Mus musculus EST BB155356.2 GI:16268254 house mouse. EST 18-OCT-2001

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VERSION
KEYWORDS
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SOURCE
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                                                                                              BB461065 660 bp mRNA linear EST 25-OCT-2001 BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-blidding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa
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RIKEN integrated sequence analysis (RISA) system--384-format
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                   nouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y. and Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified pBluescript KS(+) after bulk excision from Lambda
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/note="Girl"
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in R
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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URL:http://genome.gsc.riken.go.jp/
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                                   Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGGCCCCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laborator:
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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Second strand cDNA was
prepared with the
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25; Conserv
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This 1s the 5 sequence of the Cone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (Mational Research Centre for Biotechnology Ltd.
Braunschweig/Germany) within the cDNA sequencing consortium of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wiemann,S.)
Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                  This clone (DKFZp313J1040) is available at the RZPD in please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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 вв830730
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                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="bRFZp513J1040"
/clone_ibF="313 (synonym: hlcc2)"
/dev_stage="adult"
                                                                                                                                                                                                                                                    note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection 81 c 86 g 100 t
                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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hlcc2) Homo sapiens cDNA clone
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3. 0.0062;
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343 TACAGACCCGTGCAGACTACCTC 365
                                                            74 TACAGACCCGTGCAGACTACCTC 96
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
, Y., Ito, M., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Kojina, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Coharaki, R., Okazaki, Y., Okido, T.,
Salti, C., Sakai, K., Sahazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasumishi, A., Muramatsu, M. and Hayashizaki, Y.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bmail: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.p., Shibata,Y. Hayatsu,N. Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayyshizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S. Inoue,K. Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y., december 1982 (2001)
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Jyg-KC(B) cDNA Mus musculus cDNA clone G930013K04 3', mRNA
sequence.
BB830730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno-H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Contact: Yoshihide Hayashizaki
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                        15.0%; Score 23; DB 9; Length 438; llarity 100.0%; Pred. No. 0.071; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
//db_xref="taxon:10900"
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RCB-0527 Jyg-MC(B) CDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
108 g 96 t
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74 TACAGACCCGTGCAGACTACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
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Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
wagai,K., Fujiwake,S., Muramatsu,M., Inoue,Y., Kira,A. and
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
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/cell_line="RCB-0527 Jyg-MC(B)"
1 99 c 108 g 100 t
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/clone="G930033J21"
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                                            15.0%; >cc
100.0%; Pr
                                                                                   Score 23;
Pred. No.
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                                                  0.072;
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CV3-BN0047-150400-152-c03 BN0047
AW997058
AW997058.1 GI:8257292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; "Primates; Catarrhini; Hominidae; 1 (bases 1 to 686)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/bbrp/inage/inage.html
Insert Length: 1924 Std Error: 0.00
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Location/Qualifiers
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EST.
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                                                                            Homo sapiens
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE: 2443725"
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   Verjovski-Almeida, S., Briones, M.R.,
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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 19
High quality sequence stop: 678.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br .
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=Qv3-BN0047-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NTH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
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Laboratory of Cancer Genetics
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                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           BF239967.1 GI:11153890
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CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165
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154 c 126 g 241 t
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                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.
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o,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
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//Clones_lib="INAGE: 4133129"
//Clones_lib="INAGE: 4133129"
//Clones_lib="INAGE: 4133129"
//Lissus_type=""Iron chronic myelogenous leukemia"
//lab_host="DH10B (T1 phage-resistant)"
//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
//note="Organ: bone
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149 c 190 g 137 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
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no,S., Isogai,T.)
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281PvC04
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Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
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1. (bases 1 to 1028)
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601436060F1 NIH_MGC_72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE895133.1
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23; Conservative
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387
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/lab_host="DH10B (phage-resistant)"
/note="organ: skin; Vector: pcMy-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo of the contract of the contr
         Pv MBN #30 Plasmodium
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precursor cells"
149 c 196 g 207 t 2 others
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/db_xref="taxon:9606"
/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
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/cell_line="NT2"
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100.0%; Pr
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100.0%; Pr
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Pred. No.
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CH330-160016.TV CHORI-230 Segment
CH230-160016, DNA sequence.
Norway rat.

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                         GSS.
                                                                                                                                                                                                 вн351821
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Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today 16 (10), 409 (2000)
                                                                                                                                                                   вн351821.1
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Dept. of Pathobiology, College of Veterinary Medicine
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/dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
/note="Vector: pBluescript SK(+) vector DNA, phagemid
/note="Vector: pBluescript SK(+), infected
/note="Vector: pBluescript SK(+), infected
/note="Vector: pBluescript SK(+), and E...
/note="Vect
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497-598)"
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1 Rattus
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                                                                                                                                                                                                                                                                                                                                                                                        AGI28961
AGI289611 GI:16658126
AGI28961.1 GI:16658126
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-140E13.F.
2 (bases 1 to 838)

Rujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-Chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
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Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-160016.TJ

Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG128961 838 bp DNA linear GSS 04-NOV-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Fieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.chori.org/bacpac/or ering_information.htm]
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Matanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
a 147 c 158 g 103 t
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/clone="CH230-160016"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local.
                                                                                                                                  High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: Jwallacedu. Washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 746 row: G column: 3
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                          High quality sequence stop: 505 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome % \left( 1\right) =\left\{ 1\right\} 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 505)
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 276 c 177 g 44 t 55 others
                   /organism="Homo sapiens" (
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="PTB-140E13.F"
/sex="male"
/clone="Plate=746 Col=3 Row=G"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0314 row: M column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ486207 527 bp DNA linear GSS 05-OCT-200100314M02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0314M02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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a 77 c 107 g 119 t 5 others
                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                          adaptored DNA was purified and size-selected
                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0314M02"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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/sex="male"
                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                     /sex="Male"
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nes 19; Conserv
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                                                                                                                                                                                 electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114/gb)AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLJO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                           100.0%;
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US-08-973-363-5 153

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Scoring table:

Database :

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Total number of hits satisfying chosen

Word size : Searched:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Listing first 45 summaries
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                                                                                             SUMMARIES
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Sequence 5 from Patent WO9639505.
A58686
A58686.1 GI:3714249
                                                                                                                                                                                                                                  unclassified.
1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                                                                                                                                                                                                                               unidentified.
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Other publication AU 5906996 961224.
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A58684 Sequence 3
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AF004397 Gallus ga

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                                                                       1 (bases 1 to 1316)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                               Sequence 15 from Patent A58696
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                       unidentified
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A58685
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delta-crystallin enhancer binding
D14316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 30.7%;
l Similarity 100.0%;
47; Conservative
                                                                                                                                     Archosauria; Aves; Neognathae; Gailiformes; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 2292)

Funahashi.T
                                                                              Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (Tel:022-272-9499, Fax:022-272-3982)
                                                                                                                                                                                                                       mRNA, clone JF11.
                                                                                                                                                                                                                                                   D14316.1 GI:391639 ORF2.
                        Funahashi, J., Sekido, R., Murai, K., Kamachi, Y. and Kondoh, H. Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISIS INNOVATION (GB)
Other publication AU 5906996
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3 from Patent W09639505
A58684
               embryogenesis
                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: WO 9639505-A 3 12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/db_xref="taxon:32644"
40 c 31 g 2
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205 c 308 g
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119 (2), 433-446 (1993)
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0; Mismatches
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to. 2.9e-13;
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                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 6608)
Griffiths, R. and Tiwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A58691 6608 bp
Sequence 10 from Patent WO9639505.
A58691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 9639505-A 10 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 24.8%; Score 38; DB 5; I Similarity 100.0%; Pred. No. 9.2e-09;
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3 (bases 1 to 2292)
Funahashi,J.
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                                                                                                                       h 24.8%; Score 38; DB 6;
Similarity 100.0%; Pred. No. 7.7e-0
38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                            2289 a
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/PICOGON_STAIC=1
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/db_xref="taxon:32644"
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/note="beta-gal fusion protein binds to blocks 10 to 3 of
HN fragment of delta-crystallin enhancer."
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/tlssue_type="lens"
/clone_lib="lambda gt11"
/clone_stage="13 day embryo"
257._.1939
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6872 bp mRNA linear VRT 08-OCT-19
Gallus gallus chromo-helicase-DNA-binding on the Z chromosome
protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
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Griffiths, R. and Korn, R.M.
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AHSNQKSAACY DDYYCKWOGLEY SECSWEDGALIAKEQARIDEY FSRNGSKTPFFKD
CKYLKORF PRVALKKOPSY IGGHESELELEDYCLNGLIWLASHOCKONSCILADEWGLG
KYTJOTSFLNYLFHEHOLY GFFLLRVPLSTLTSWOREIGTWAP OMNAVYLGDITSRN
MIRTHEMMHPOTKRLK PULLITTY EILLKDK SFLGGLMAR I GYDEBHKKER LADEWGLG
KYTLOTSFLNYLFHEHOLY GFFLLRVPLSTLTSWOREIGTWAR PIGVDEARFLKNDDSLLY
RTLIDEKSKHIRFLLTGTPLQNSLKELEWSLLHF IN PEKF SSWEDFEEBHKKER KYRKOSK
STSGFLNIMMELKKCHNCYLIK FELWSLLHF IN PEKF SSWEDFEEBHKKER KOSK
STSGFLNIMMELKKCHNCYLIK PEDDDNEFYNKOBALOHGYYKNITRNYKALSKOSK
STSGFLNIMMELKKCHNCYLIK PEDDDNEFYNKOBALOHGYKOVNIY RLVTYKG
STSGFLNIMMELKKCHNCYLIK PEDDNAFYNKOBALOHGTRASGKLILLDKLLIRLR
ERGNRVLIFSGMYKANDLLADLABETLK TROFF ORLDGS KGELRKOALDHFNAEGSEDFC
FLLSTRAGGLGINLASADTVY IFDSDMAPONDLOAQARAHRIGOKOVNIY RLVTYKG
VEEDILERAKKKHVLDEILY ORDOTTGKTVLHFGSTPSSTPENKEELSALLKGAEE
LFKEPEGEEOEPOEDILD EILKRAETRENEPGPLTVLDELLSQFK VANFSNADEDDIE
LEBERNSRNWEEI IFESGR RRIEBEEROKELEEI TWL.PRKNRCKKOVKOKOVNIY RLVTYKG
VEEDILERAKKKHVLDSLLVORDTGKTVLHGSSDAEER RET KSYKKFGOEDENLLVG
OVNAKLV ISHEEELAPLHKS IPSDPEERK FVLTDCHTKAAHEDIDMGKEDDSNLLVG
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OVNAKLV ISHEEELAPLHKS IPSDPERK FVLTDCHTKAAHENDLDRAKEAO
ORLAGAONSKRRKTBNKKKKKASKIKEELKSDSSOOPSEKSDEDDEEEDNKEFLKEN
KEYTNPEQIKQWRKNLWIFYSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNYN
THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mnghsdeesvrnssgessrsdddsgsasgsgsgsgssssdsssdgss
sqsgssbsesgsesgsosesesdtsrekkqvqakppkadgsefwksspsilavqrsav
                                                                            NKEKRENKVKESTOKEKEVKEEKVNEMKSENKEKSKKIPLLDTPVHITATSEPVPISE
ESEELHOKTFSVCKERMRPVKAALKOLDRPEKGLSEREOLEHTROCLIKIGDHITECI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
/codon_start=1
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                                                                                                                                                        HLHKKIKTEKENEEKPEPDIGIKKEAEEKRETKEKENKRELKREKKEKEDKKELKEKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC60282.1"
/db_xref="GI:2501846"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="chromo-helicase-DNA-binding on the Z chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9031"
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SOURCE
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                                             RESULT
BC009024
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                                                                                                           835
                                                                                                                        111 TAAAGACCTTGCAAGAAAAGA 131
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                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hay, J.C., Chao, D.S., Kuo, C.S. and Scheller, R.H. Protein interactions regulating vesicle transpot endoplasmic reticulum and Golgi apparatus in mam cell 89 (1), 149-158 (1997) 97248495
BC009024 1339 bp mRNA linear ROD 12-JUL-20 Mus musculus; SEC22, vesicle trafficking protein (S. cerevisiae)-like 1, clone MGC:5885 IMAGE:3481731, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 959)
Hay,J.C., Chao,D.S., Kuo,C.S. and Scheller,R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-FEB-1997) Molecular University, B155 Beckman Center, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                            /translation="MYLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKL NEQSFPRCTLEAGAMTEHYILEQGVCYLVLCEAAFPKKLAFAYLEDLHSSEDEGHGKK VPTVSRPYSFIEFDTETQKTKKLYLDSRARRNLGSINTELQDVQRIMVANIEEVLQRG EALSALDSKANNLSSLSKKYRQDAKYLMRSTYAKLAAVAVFFIMLIVYVRFMML"

219 c 261 g 238 t
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/note="short insert
1223 c 1520 g
                                                                                                                                                                                                                                                                                                                                     /product="vesicle trafficking protein sec22b"
/protein_id="AAC53130.1"
/db_xref="GI:1907386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1907385
                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Sec22"
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                    13.7%;
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; Pred. No.
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Pred. No.
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1683
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7.7e-09;
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Stanford, CA 94305, USA
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                                                                                                                                                                    0;
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; Murinae; Mus
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A, complete cds.
                               ROD 12-JUL-2001
                                                                                                                                                                    0;
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BC001364
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                                                                                                                                            Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 6 Row: k Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1907385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Huly)
A.M., Holloway, M., Telford, B, Hodgson, A.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump)
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
  Homo sapiens, SEC22, cerevisiae)-like 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-MAY-2001) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Bethesc
                                           BC001364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1339)
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BC009024.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                                                                       347
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                  /translation="MYLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKL
MEQSFPRCTLEAGAMTEHYILEQGYCYLVLCEAAFPKKLAFAYLEDLHSEFDEQHGKK
VPTVSRPYSFIEFDTFIQKTKKLYIDSRARRNLGSINTELQDVQRIMVANIEEVLQRG
EALSALDSKANNLSSLSKKYRQDAKYLNIRSTYAKLAAVAVFFIMLIVYVRFMWL"
a 291 c 344 g 357 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="SEC22, vesicle trafficking protein
cerevisiae)-like 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="LocusID:954"
/db_xref="taxon:10090"
/clone="MGC:5885 IMAGE:3481731"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAH09024.1"
/db_xref="GI:14290512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                13.7%;
100.0%;
1491 bp mRNA linear PRI SEC22, vesicle trafficking protein (S. ike 1, clone MGC:1960 IMAGE:3051087, mRNA,
                                                                                                                                                                                                                           0;
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Pred. No.
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3.9
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hodason, A., Bouck,
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                                                                                                                                                                                                                                                                   Length 1339;
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                                              PRI 12-JUL-2001
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ı, W.,
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VERSION
RESULT 11
                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                        111 TARAGACCTTGCAAGAAAAGA 131
                                                                       889 TAAAGACCTTGCAAGAAAAGA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: c Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 3335139. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaithersburg, Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                    428 a
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                          /Product="SEC22, vesicle trafficking protein (S. cerevisiae)-like 1"
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EALSALDSKANNLSSLSKKYTODAKXLMMRSTYAKLAAVAVFFIMLIVYVRFWML"
a 289 c 342 g 432 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MGC:1960 IMAGE:3051087"
//tissue_type="Skin, melanotic melanoma."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                     13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ector: pOTB7"
                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                     Score 21;
Pred. No.
                                                                                                                                                                                                     3.8;
                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                              Length 1491;
                                                                                                                                                                            Gaps
                                                                                                                                                                            0;
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AUTHORS
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Query Match
Best Local Similarity
25083 TAAAGACCTTGCAAGAAAAGA 25103
                                                                            111 TAAAGACCTTGCAAGAAAAGA 131
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On Sep 14, 2001 this sequence version replaced gi:1389736. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submitssion corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SWISSEROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl RP11-544024 is from the library RPCI-11.2 constructed by the group of Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RP11-544024 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-544024 is at 1 in this sequence. The true left end of clone RP4-646P11 is at 85737 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL359758 85836 bp DNA linear PRI 13-SEP-2001
Human DNA sequence from clone RP11-544024 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 85836)
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                                                                                                                                                                                                                                                                                                                                                                                             /note="Single clone region. Assembly confirmed by restriction digest data." 25942 a 1696 c 16876 g 26032 t
                                                                                                                                                        13.7%; Score 21; DB 9; ilarity 100.0%; Pred. No. 1.9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-544024"
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30369 ...30381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/chromosome="1"
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                                                                                                                                                                                                                                    Length 85836;
                                                                                                                                                        0;
                                                                                                                                                             0;
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KEYWORDS SOURCE

COMMENT

JOURNAL

AL391556 LOCUS

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REFERENCE
AUTHORS
TITLE
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VERSION
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Sequencing vector: plasmid; LO875; 100% of reads
Chemistry: Dye-terminator ET-amersham; 43% of reads
Chemistry: Dye-terminator ET-amersham; 43% of reads
Chemistry: B6114 bases at least 040
quality: 86114 bases at least 040
quality: 86114 bases at least 040
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Center code: SC
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* This record will be updated with the finished sequence.
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95178 bp DNA linear HTG 10-JUL-2001
Homo sapiens chromosome 1 clone RP4-630J2 map q21.1-21.3, ***
SEQUENCING IN PROGRESS ***, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coverage: 2.64x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
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                              50595 50694: gap of 100 bp 50695 53552: contig of 2658 bp in length 5353535352: gap of 100 bp 53453 61187: contig of 7735 bp in length 61288 65569: contig of 3782 bp in length 65070 65169: gap of 100 bp 6570 65169: gap of 100 bp 6570 69334: contig of 3782 bp in length 69335 69434; gap of 100 bp in length 69335 69435 gap of 100 bp in length 69335
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37253 443
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27069
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3064 3163: gap of 100 bp
3164 6176: contig of 3013 bp in length
6177 6276: gap of 100 bp
6277 9333: contig of 3057 bp in length
9334 9433: gap of 100 bp
        69434: ga
77503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9333: contig of 3057 bp in length

9433: gap of 100 bp

18624: contig of 9191 bp in length

18724: gap of 100 bp

26968: contig of 8244 bp in length

27068: gap of 100 bp

37152: contig of 10084 bp in length
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46867: -
                                                                                                                                                                                                                                                                                                                                                                              367: gap of 100 bp
50594: contig of 3627 bp
594: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52: gap of 100 bp 44300: contig of 7048 bp in
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fragment_chain:1"
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86697. .92135
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77604. .79864
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fragment_chain:2"
18725. .26968
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fragment_chain:1"
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/clone="RP4-630J2"
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E 2 (bases) 1 to 144979)

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

B Birven, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Brown, A., Castle, A., Colangelo, M., Dondino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lleu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughilin, J., Meldrin, J.,

McEwan, P., McGurk, A., McKernan, K., McLaughilin, J., Meldrin, J.,

Morrow, J., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassilite, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This record contains 138 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, Clone RP11-20N19
Unpublished
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HOMO Sapiens clone RP11-20N19, LOW-PASS SEQUENCE SAMPLING.
ACO16280
ACO16280.3 GI:9123976
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                            871 971: contig of 871 bp in length 172 971: gap of 100 bp 172 1881: contig of 910 bp in length 1882 1981: gap of 100 bp 1882 1985: contig of 888 bp in length 1882 2969: contig of 888 bp in length 1880: contig of 911 bp in length 1881 3980: gap of 100 bp 3981 4853: contig of 873 bp in length
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11852: 11951: gap of
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                  200 2192: gap of 100 bp 11 le 132 22937; gap of 100 bp 10 le 133 22937; gap of 100 bp 10 le 133 22937; gap of 100 bp 10 le 133 23912; gap of 100 bp 10 le 133 23912; gap of 100 bp 10 le 2575; contig of 807 bp in le 158 2587; gap of 100 bp 2575; contig of 807 bp in le 158 2587; gap of 100 bp 2575; contig of 907 bp in le 158 2587; gap of 100 bp 10 le 159 2589; contig of 907 bp in le 159 2589; contig of 807 bp in le 159 2589; contig of 807 bp in le 159 2589; contig of 807 bp in le 158 31857; gap of 100 bp 10 le 159 2589; contig of 807 bp in le 159 2579; contig of 807 bp in le 159 2579; contig of 807 bp in le 159 2579; contig of 807 bp in le 150 bp 10 l
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13796: con
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1776: gap of 100 b
39679: contig of 900 b
9779: gap of 100 br
40654: contig of 875
10754: gap of 100 b
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63476: contig of 843 bp 1
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64458: contig of 882 bp in
1558: gap of 100 bp
165442: contig of 884 bp in
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55500: contig of 872 bp in 1e

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5603: contig of 903 bp in 1e

6603: gap of 100 bp

57517: contig of 914 bp in 1e

57617: gap of 100 bp

57617: gap of 100 bp

58500: contig of 883 bp in 1e
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43575: contig of 916 bp
3675: gap of 100 bp
44570: contig of 895 bp
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45577: contig of 907 bp
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0611: gap of 10
51543: contig of 9
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71850: contig of
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72978: contig of
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587: gap of 100 b
61508: contig of 921
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577: gap of 100 bp
46590: contig of 913 bp in
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                                                                                                                                                                                                                                                             AUTHORS
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HTG.
                                                                                         Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Jan 9, 2002 this sequence version replaced gi:14165368.
                                                                                                                                                                                                       Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                        3 (bases 1 to 149462)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 149462)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens BAC clone RP11-470J24
                                                                                                                                                                 Waterston, R
                                                                                                                                                                                               мо 63108,
                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                Toward a complete human genome Genome Res. 8 (11), 1097-1108 (
                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                     Nguyen,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                 (bases 1
               Contact: sapiens@watson.wustl.edu
Center project name: H_NH0470J24
                                                             Center: Washington
Center code: WUGSC
                                             Web site: http://genome.wustl.edu/gsc
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Eutheria; Primates;
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                                                                                                                                                                                 to 149462)
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                                                                           University Genome
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(1998)
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                                                                                                                                                                                                                                                                                                       clone RP11-470J24
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from 2,
                                                                                                                     St. Louis, Missouri 63108,
                                                                         Sequencing Center
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                                                                                                                                                                                                                 Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Mo. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc MAPPING INFORMATION:) D. et. Louis

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) SOURCE INFORMATION: The RPCI-11 human B NEIGHBORING SEQUENCE INFORMATION: pBACe3.6

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136773

AAAGACCTTGCAAGAAAAGAA 136793

clone sequenced
clone sequenced to the left is RP11-310K15, to the right is RP11-156A1, 2000 dq qd overlap;

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misc_feature
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/chromosome="2"
/map="2"
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9974. .10197
                                /rpt_family="(TTG)n"
9685...9973
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7982. 8006
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)65. .1037
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1486. .3527
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1. .4273
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4. .2844
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 ACCESSION
VERSION
                                           RESULT 15
AC024119
LOCUS
DEFINITION
                                                                                                                                       Db 111213 AAAGACCTTGCAAGAAAAGAA 111233
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ACO24119 150436 bp DNA linear HTG 12-OCT-2000 HOMO sapiens chromosome 3, WORKING DRAFT SEQUENCE, 22 unordered pieces.
ACO24119 GI:10305055
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21366. .2168
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KEYWORDS
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AUTHORS
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 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 150436)

Xu,S., Zhao,Y., Lin,W., Dong,H., Wan,M., Zhang,C., Gu,W., Tu,Y.,
Jia,J., Wu,C., Lu,G., Zhong,M., Zhou,Y., Ren,S., Fu,G., Chen,Z. au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact:hgc@igtp.ac.cn.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 22 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code:Beijing
Website:http://hgc.igtp.ac.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genomics.org.cn
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В
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ORIGIN
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91838 TAAAGACCTTGCAAGAAAAGA 91858
            111 TAAAGACCTTGCAAGAAAAGA 131
                                                                                                                   45301
                                           13.7%; Sullarity 100.0%; If a conservative 0;
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                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone_lib="542|23"
a 29770 c 31151 g 44136
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Search completed: August 3, 2002, 01:43:18 Job time: 40768 sec

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Result
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                                                                                                                                                                                                                                                                                                                                                                               Score
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                           Great tit CHD-W gene f Chicke CHD-W gene f Chicken CHD-W gene Chick CHD-1A gene Chicken CHD-1A gene Human CHD-Human 
                                                                                                                                                                                                                                                                                                                                                                                   Description
Arabidopsis thalia
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(ISIS-)	י ה	12-DEC	W09639	Key misc_d	Parus	Bird; CHD-1A	Great	12-MAR-	AAT42759	3ULT 1 342759 AAT427		44	43	4	39 40	38	36	ω ω 4	33	32	29 30	28	26	24 25	23	21	19 20	18	16	15	ω (11	10
SISI (1996	-1996.	505-A1	liffere	major.	sex dete	tit CHD-	-1997	59;	59 sta										16													
INNOVATION	96WO-		•	rence 52 /* /n		≈ ∄.	D-W gene	(firs		andard;							•			10.5									•		4.	•	
<u></u>	GB01			Location 5281 /*tag= /note= "		nation; ch chromosome		t entry)		DNA;		699	699	690	690	681	634	630	594	537	537	537	3 8 5	196 351	136	5647	2395 5647	1788	3225	1580	44861	2580	1160
LTD.	341.			/Qua a bases and a acid		chr ome;	fragment	۲)		153										22													
				/Qualifiers a bases 52-81 are a repe and are ignored in the acid sequence given in		chromodomain-Helicase- me; ss.	τ.			₿₽.	ALIGNMENTS	AAQ47363 AAQ70192	AAQ20236	AAQ70191	AAQ47362 AAQ70209	AAQ4/369 AAQ70201	AAS93365	AAQ47367 AAQ70199	AAK93548	AAI41060 AAK91625	AAK09455 AAK35347	ABA61160	AAF67429	AAV78976 AAO45230	AAQ74182	AA163751	AAC43194 AAI99401	AAZ56344	AAV20467	AAF 00219 AAF89129	AAS20000	AAZ98313	AAC34655
				eat of bases 22-51 e translated amino n Fig 3"		e-DNA binding 1;						Sequence encoding Sequence encoding	Encodes var(1) co	Sequence encoding	Sequence encoding	sequence encoding	DNA encoding novel	Sequence encoding Sequence encoding	Human cDNA clone r	Probe #9746 used t	Human brain expres Human bone marrow	Human foetal liver	Novel human polynu	Staphylococcus aur Partial sequence o	5' end fragment of	Human kidney relat	Arabidopsis thalia Human excretory re	Escherichia coli f	Human c-myb oncoge	Human homoglutamin	DNA encoding pyrid	A. thaliana gene i Human polynucleoti	Arabidopsis thalia

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Matches 138; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian
birds
                                                                                                                                                                              misc_difference
        Griffiths
                                                  06-JUN-1995;
                                                                       05-JUN-1996;
                                                                                                                 WO9639505-A1
                                                                                                                                                                                                                                             Bird;
                                                                                                                                                                                                                                                               Chick CHD-W
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                             (ISIS-) ISIS
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                                                                                                                                                                                                                                          sex determination; chromodomain-Helicase-DNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
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                                                                                                                                                                                                                                                               gene fragment.
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                                                                                                                                                                             Location/Qualifiers 52..81
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and are ignored
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                                                                                                                                             a repeat of bases in the translated
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Best Local
       The chicken CHD-W gene (AAT42754) acting alone or in conjunction wit the closely related CHD-1A gene (AAT47751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian
birds
                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                     CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken
                                                                                                                                                  Claim
                                                                                                                                                                                                                                              Griffiths
                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                 W09639505-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT42754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT42754 standard; cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153 BP; 56 A; 36 C; 31 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW08148
                                                                                                                                                                                                                                                                       (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                        12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                   1997-043127/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagacccgtgcagattacctcattaaattactgaataaagaccttgcaagaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromodomain-helicase-DNA binding genes determine sex
- used for sex determn. and to control sex of progeny
                                                                                                                                                  1;
                                                                                                                                                                          chromodomain-helicase-DNA binding genes determine sex used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                            sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                  sex determination; chromodomain-Helicase-DNA binding 1 chromodomain-Helicase-DNA binding on the W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHD-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                               Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 3; 76pp;
                                                                                                                                                                                                                                            Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                              8; 76pp;
                                                                                                                                                                                                                                                                         INNOVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                            Tiwari
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                                                                                                                                                                                                                                                                                                                             96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.6%;
                                                                                                                                                 English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 T; 0 other;
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2.8e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                     Query Match
Best Local :
                                                                                                                                  Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42759) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-14 (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chick CHD-1A gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1189 cgtgcagattacctcattaaattactgaataaagaccttgcaagaaa 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                    Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                      Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bird; sex determination; chromodomain-Helicase-DNA binding
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                                                                                                          Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                            Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                                                                              WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 CGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0%; nes 47; Conservation
91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                     Similarity
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                                        Conservative
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                                                   24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 2.9e-14;
                                                     Score 38;
Pred. No.
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                                                                 DB 18; Length 153;
                                                      le-09;
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                                        Indels
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RESULT
AAV49574
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                                                                                                                               4140 tacctcattaaattactgaataaagaccttgcaagaaa 4177
                                                                                                                                                                                                                                                                                 The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken CHD-1A gene
                                                        AAV49574 standard; cDNA to mRNA; 1409
                                                                                                                                                                                                                                                            Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffiths R, Tiwari B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian;
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21-OCT-1998
                            AAV49574;
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                                                                                                                                           91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128
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                                                                                                                                                                                   Local Similarity es 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromodomain-Helicase-DNA binding on the W chromosome; ss
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
(first entry)
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                                                                                                                                                                                                   24.8%; Score 38;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8099
                                                                                                                                                                                       0;
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                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                   DB 18;
. 1e-09;
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AAX56240
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Matches 21
                                                                                                                                                                                                                                                                                                            AAV49550-V49599 are cDNA sequences which encode human proteins containing a transmembrane domain. These proteins can be used for, e.g. research and nutrition, and may have cytokine and cell proliferation/differentiation, immune stimulating/suppressing, haematopoiesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand,
          W09921988-A1
                                              Human; vesicle trafficking protein; SEC22b; CBFBBA01; cancer; autoimmune disease; diabetes mellitus; multiple sclerosis; diagnosis; ss.
                                                                                      Human CBFBBA01
                                                                                                                                                AAX56240 standard;
                                                                                                                                                                                                                                                                                    Sequence 1409 BP;
                                                                                                                                                                                                                                                                                                      anti-inflammatory or
                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 153-155; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane domain; human; nutrition; cytokine; cell proliferation; differentiation; immune system; stimulator; suppressor; regulator; heamatopoiesis; activin; inhibitor; chemotactic; chemokinetic; recept
                                                                                                         16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                     Human protein having transmembrane domain - research and nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09821328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lymphoma cell line U937 clone
                             Homo sapiens
                                                                                                                                                                                                842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGA)
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                                                                                                                                                                                                                 111 TAAAGACCTTGCAAGAAAAGA 131
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                                                                                                                                                                                              1998-297932/26
DB; AAW64546.
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SAGAMI CHEM RES CENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kobayashi M,
                                                                                                                                                                                                                                     Conservative
                                                                                                        (first entry)
                                                                                    vesicle trafficking
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "transmembrane domain containing protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                  377 A; 278 C; 325 G; 429 T; 0 other;
                                                                                                                                               cDNA; 1462
                                                                                                                                                                                                                                            13.7%;
                                                                                                                                                                                                                                                                                                      tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sekine S,
                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                             Score 21;
Pred. No.
                                                                                                                                                ВP
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamaguchi
                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HP10136 cDNA
                                                                                                                                                                                                                                             0.38;
                                                                                                                                                                                                                                                      DB 19;
                                                                                     SEC22b
                                                                                                                                                                                                                                                                                                                                                                                                              useful for,
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                      Length 1409;
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                                                                                                                                                                                                                                    0;
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AAT11338
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Matches
23-JUN-1994;
                  22-JUN-1995;
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine vesicle trafficking protein sec22b. CBFBBA01 is a cytoplasmically-orientated integral membrane protein, located in the endoplasmic reticulum and golgi membranes. CBFBBA01 polynucleotide (I), vectors containing (I) and recombinant host cells are useful for recombinant production of CBFBBA01. Both (I), CBFBBA01 and antibodies against CBFBBA01 are useful as research reagents, for screening assays and in diagnostic assays, especially for cancer, autoimmune disease, diabetes mellitus and multiple sclerosis. Antagonists and agonists of CBFBBA01 can be used to inhibit or enhance, respectively, the activity of CBFBBA01 or expression of (I). Anti-CBFBBA01 antibodies and CBFBBA01 or its fragments can be used in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBFBBA01
diabetes
                             24-JAN-1996
                                                           EP693554-A1
                                                                                                                                                                                     Arabidopsis
                                                                                                                                                                                                                  plant;
                                                                                                                                                                                                                                 signal
                                                                                                                                                                                                                                                               Arabidopsis fourteen-three-three 1; AFT1; Cruciferae; regulation;
                                                                                                                                                                                                                                                                                           AFT-1 interacting protein (partial ascorbate peroxidase) cDNA.
                                                                                                                                                                                                                                                                                                                             05-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes CBFBBA01, which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 21; 29pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein useful in treating cancer, mellitus and multiple sclerosis
                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                       /*tag= a
/product= partial_ascorbate_peroxidase
/note= "plant defence related protein"
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2..370
                                                                                                                       /*tag=
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                                                                                                                                                                                                                                  defence
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                                                                                                                                                                                                                                                 gene expression modulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMT11338 encodes a partial ascorbate peroxidase, a plant defence-related protein (PDRP). AMT11338 and other cDNA molecules encoding PDRPS were isolated using a Lexa/AFT1 33-194 fusion protein i.e. AFT1 (Arabidopsis 14-3-3 1) protein residues 33-194 fused to LexA, a DNA binding protein, in an interaction trap assay. AFT1 is a transcriptional activator protein and may be used to enhance, control or modify plant gene expression, e.g. in the regulation of plant storage components (esp. napin, Legumin or phaseolin). AFT1 can also be used to modulate signal transduction events involved in plant defence responses to pathogens such as fungi, nematodes, and plant defence responses to pathogens such as fungi, nematodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                    25-FEB-2000;
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                          The invention relates to isolation of coding sequences and/or genes involved in tolerance to environmental stress in plants. The sequences (AAZ98305-Z98365) are useful for producing a transgenic plant having enhanced tolerance or resistance to environmental stress conditions such as anaerobic, flooding, cold, dehydration, drought, heat stress or salinity. This is useful for producing improved yield, growth, development and productivity under environmental stress conditions, and also provides growth of crops in areas where they cannot grow without the induced osmotolerance. Sequences AAZ98305-365 represent polynucleotide sequences from A. thaliana that are involved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ98313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ98313 standard;
                   environmental stress
                                                                                                                                                                                                                                      Lee JH,
                                                                                                                                                                      isolating
                                                                                                                                                                                Isolation
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                                                                                                                                                                                                      2000-205726/18.
DB; AAY77933.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                  Page 112-115;
                                                                                                                                                                                                                                     Verbruggen
                                                                                                                                                                      of polynucleic genes involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      drought;
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990S-01
990S-01
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S-0161992.
S-0161993.
S-0162142.
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S-0161405.
S-0161406.
S-0161359.
S-0161360.
S-0161361.
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                    tolerance.
                                                                                                                                                                                                                                                                                                                                                                                     plant; transgenic plant; anaerobic; flooding; cold; heat stress; salinity; osmotolerance; ds.
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                                                                                                                                                 312pp; English.
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                                                                                                                                                                      acids useful 
in tolerance
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                      to e
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                                                                                                                                                                      environmental stress
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                                                                                                                                                                                producing transgenic
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BP;

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459

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544

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T; 0 other

disorders

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Best Local Similarity
Matches 20; Conser
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Inmune system suppression, activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and the control of the activity acceptance.
                                                                                                                                                                                                                                                                                                 Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                      Claim
                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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            assays
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokinetic; thrombolytic; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID
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DB; AAM39821.
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            for receptor
                                                                                                                                                                                                                                                                                                                                      HYSEQ INC
                                                                                                                                                                                                                                                                                    Wang Z,
Zhou P,
                                                                                                                                                                                      SEQ ID NO 1180;
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman
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                                                                                                                                                                                                                                                                                     Goodrich R,
           activity,
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Xu C,
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Pred. No.
            arthritis and
                                                                                                                                                                                                                                                                                     len R, Ma
lu C, Xue
Drmanac F
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e AJ,
RT;
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Yang
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              leukaemias
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E.L.	FT variation	EL L	FT variation		FT intron	FT exon		FT intron	FT exon		FT intron	FT exon	FT Variation		FT intron	FT exon	E.L.	FT (000		FH Key FT variation	OS Homo sapiens.	<pre>KW autoimmune po KW gene therapy; XX</pre>	<pre>KW Pyridoxal kinase;</pre>	DNA encoding	26-MAR-2002	AAS20000;	000	RESULT 13	Db 1776 tgatgaco	Matches	Query Match Best Local Similarity	SQ Sequence 2532	CC Note: The seq CC specification
/*cag* m /standard_name= "Single nucleotide polymorphism"		/*tag= 1 /standard_name= "Single nucleotide polymorphism"	replace(28631,G)	/*tag= k	/number= 4 28606 . 30876	2852228605 /*tag= j	/number= 3		, h	/"umber	464	9921	replace(422,") /tag= e /taga e /standar name= "Gingle nucleotide rolumorrhism"	/ number = 1	= 7	4093.4179 CTAINED IN CIGIN 2/	yridoxine	/stag= b /stag= b /stag= b	/*tag= a /standard_name= "Single nucleotide polymorphism" /003 /0661	Location/Qualifiers replace(3930,G)		andular disease type 1; tomosome 21q22.3; ds.	se; pyridoxine; vitamin B6; PDXK	pyridoxal (pyridoxine, vitamin B6) kinase (PDXK).	(first entry)		standard: DNA: 44861 BP.		Teatement Andrea 2/	0; Mismatches 0; Indels 0; Gaps 0;	12.4%; Score 19; DB 22; Length 2532; 100.0%; Pred. No. 3.9;	BP; 648 A; 654 C; 688 G; 542 T; 0 other;	sequence data for this patent did not form part of the printed :ion.
FT variation FT		FT exon		FT variation		FT intron	FT Variation		FT exon	FT VALIACION		FT intron	FT exon		FT variation	FT variation FT		FT variation	FT intron	FT exon FT			FT variation	19 P. P.	FT intron	FT variation FT		FT variation	FT variation	FT exon	FT variation FT	FT intron	FT exon
replace(40516,C) /*tag= ak	/number 10		<pre>/*tag= ai /standard_name= "Single nucleotide polymorphism"</pre>	0,	/*tag= ah	. a	replace(3839/,T) /*tag= ag	/number= 9	:. =		/number o /cons_splice=(5'site:YES,3'site:NO)		27	<pre>/*cag= ab /standard_name= "Single nucleotide polymorphism"</pre>	0 2	/standard_name= single nucleotide polymorphism: replace(37287,A) /*tag= aa		/^ Lag=		•	<pre>/*tag= w /*tagard name= "Single nucleotide polymorphism"</pre>	<pre>/*tag= '\ /*tag= '\ /*standard_name= "Single nucleotide polymorphism" replace(s5202.6)</pre>	<pre>/cons_splice=(5'site:NO,3'site:NO) replace(33922,G)</pre>	/number= 6)	"Single pucleotide	<pre>/ rcuy / rcuy / rcuy / rcuy / rcuy / rstandard_name= "Single nucleotide polymorphism" / replace(33831,G)</pre>	/*tag= q /number= 6 replace(33801,A)	: 2	776,C)	3092433792 /*tag= 0	3087730923 /*tag- n /numbor- s

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                                                                                                                                                       The invention describes an isolated human pyridoxal (pyridoxine, vitamin CC B6) kinase, (PDXX) polynucleotide. The polynucleotide is useful in CC studying the expression and function of PDXK, and in expressing PDXK CC protein for use in screening for candidate drugs to treat PDXK related CC diseases and for therapeutic purposes. A transgenic animal is useful for CC studying expression of the PDXK isogenes in vivo, for in vivo screening CC and testing of drugs targeted against PDXK protein, and for testing the CC efficacy of therapeutic agents and compounds for autoimmune polyglandular CC disease type 1. The polypeptide is useful for studying the effect of the CC variation on the biological activity of PDXK and the binding affinity of C2 candidate drugs targeting PDXK for the treatment of autoimmune CC polyglandular disease type 1. Genotyping and haplotyping is useful for CC polyglandular disease type 1. Genotyping and haplotyping is useful for CC improving the efficacy and reliability of several steps in the discovery CC and development of drugs for treating disease associated with PDXK CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK CC as a candidate agent for treating a specific condition or disease CC predicted to be associated with PDXK activity, and in the design of CC clinical trials of candidate drugs. This sequence (located on chromosome CC 21922.3) encodes human pyridoxal (pyridoxine, vitamin B6) kinase (PDXK) and forms the reference sequence on which the isoforms AMU11922 and CC AMU11953 are based, described in the method of the invention.
                                                                 Query Match
Best Local S
Matches 19
1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chew
                                                                                                                                                       Sequence 44861 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts. useful for therapeutic purposes, for studying the expression and function of the polyNt, and for expressing pyridoxal protein -
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                                                                  Local Similarity
les 19; Conser
ccaagaaaccacaggcaaa 1850
                                CCAAGAAACCACAGGCAAA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duda A,
                                                                 Conservative 0;
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replace(40875,C)
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/*tag= am
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replace(40521,T)
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                                                                                                 Score 19;
                                                                                   Pred.
                                                                  Mismatches
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                                                                                                                                                     13398 G;
                                                                                 3.8;
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                                                                 0;
                                                                                                 Length 44861;
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                                                                 0;
                                                                 Gaps
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RESULT

Matches

18;

Conservative

0;

Mismatches

0,

0

Gaps

0;

Query Match
Best Local Similarity

11.8%; Score 18; 100.0%; Pred. No.

DB 22; 13;

Length 552; Indels

Sequence

552

BP;

220

A,

118

ç;

69

G; 144

H ,,

1 other

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CC associated proteins (I) and the nucleic acids (NAS) that encode them.

CC (I) have cytostatic activity and can be used in gene therapy, antisense conhibition and in vaccines. The NAS and the lung tumour-associated proteins they encode may be used in the prevention, treatment and concers. For example, the NAS may be administered to treat diseases by rectifying mutations or delections in a patient's genome that affect the activity of the protein by expressing inactive proteins cor to supplement the patients own production of (I). Additionally, the CC NAS may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in cassays to detect and quantitate the presence of similar NA sequences in cassays to detect and quantitates may be in need of treatment for lung cancer. The (I) may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the captesion and activity of the protein. AAP68083 to AAF6878 and antagonists in the protein related conclection and protein sequences which are used in the exemplification of antibodies and the present inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T, Ba
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes immunogenic portions of lung tumour-
associated proteins (I) and the nucleic acids (NAs) that encode them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-2000;
22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 193; 436pp; English.
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17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer
                                  present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bangur CS,
Wannion
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2000US-0533077.
2000US-0546259.
2000US-0560406.
2000US-0589184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; lung tumour; lung tumour protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US18061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0419356.
99US-0466867.
99US-0476300.
                                    invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung tumour-specific antigen; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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AAF89129
                                                            Ouery Match 11.8%; Score 18; DB 22; Length 1580; Best Local Similarity 100.0%; Pred. No. 13; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                 The present invention provides the protein and coding sequences of human homoglutamine-rich factor 56 (HQRF). This is useful in the treatment of cancer, anglocardiopathy, nervous system diseases, immune diseases and phlogosis. The present sequence is the homoglutamine-rich factor 56
                                                                                                                                                                                                                                                                                             Homo (human) glutamine(Q)-rich factor 56 applicable in diagnosis and treatment of cancer, anglocardiopathy, nervous system diseases, immune diseases and phlogosis \,\cdot\,
                                                                                                                                       Sequence 1580 BP; 463 A; 444 C; 346 G; 327 T; 0 other;
                                                                                                                                                                                                                                                                   Claim 6; Page 21-22; 29pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-281976/29.
P-PSDB; AAB83299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2000; 2000WO-CN00310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; homoglutamine-rich factor 55; HQRF; cancer; angiocardiopathy; nervous system disease; immune disease; phlogosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human homoglutamine-rich factor 56 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                            Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-1999; 99CN-0116946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200127148-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "homoglutamine-rich factor 56"
                                                              0;
                                                              Gaps
                                                              0;
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Search completed: August 3, 2002, 01:50:11 Job time: 32196 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM nucleic -
                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                 Score
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153
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Copyright (c) 1993 - 2000 Compugen Ltd
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em_htc:*
gb_est1:*
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em_gss_inv: *
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                   BE842996 MR4-ST024
A354813 EST63335
BF289372 EST45963
A1902726 QV-BT011-
AA234796 ZT78C05.r
BG66575 DRABNG04
BB6575124 602594129
BM6575124 602594129
AW464649 BP230016A
BE198840 Ug79905.y
AW579514 MR0-HT016
BM72916 MR254
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KEYWORDS
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                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR4-ST0240-240
700-013-e10&t3=2000-07-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 167.
1. 167
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 167)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bah,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                       ввич 2996
MR4-ST0240-240700-013-e10 ST0240 Homo sapiens cDNA,
BE842996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                 Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                             Simpson, A.J.
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1. .16/
/organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW992921
AW958448
D BM229259
AW992919
AW993201
AW993283
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AW993201 RC2-BN003

AW993281 RC2-BN003

AW993287 RC2-BN003

AW993467 RC2-BN003

AW993461 RC2-BN003

AW993461 RC2-BN003

AW993471 RC2-BN003

BN093471 AW9327373

BN0947442 RW947474

AW996787 QW3-BN004

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                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAGACCTTGCAAGAAAGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 314)
                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: THC180658
                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                            Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                        Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue mRNA and cDNA amplification were performed under low stringency conditions." 42 \ c \qquad 29 \ g \qquad 58 \ t
/db_xref="ATCC (inhost):155260"
/db_xref="taxon:9606"
                                                  /organism="Homo sapiens"
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/clone_lib="ST0240"
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                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAGACCTTGCAAGAAAAGA 81
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AI902726 355 bp mRNA linear EST 30-
QV-BT011-101198-028 BT011 Homo sapiens cDNA, mRNA sequence
AI902726
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                        /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                               /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                         norvegicus cDNA"
                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RRIHE60"
/clone_11b="Rat Gene Index, normalized
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1.3;
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                                                                                                                                                                                                                                                        438 bp mRNA linear EST 05-AUG-1997 zr78c05.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:669512 5', mRNA sequence.
AA234796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2/V/V-L
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 355)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baha, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 438)
1 (bases 1 to 438)
1 (bases 1, Martin, M., Bowles, L., Dubque, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Bowles, L., Lenon, G., Marra, M., Martin, J., Moore, B. Kucaba, T., Lacy, M., Leanon, G., Marra, M., Martin, J., Woore, B. Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer:
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                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                         AA234796.1 GI:1859289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="BT011"
/sex="female"
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1. .355
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/db_xref="taxon:9606"
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homninidae; Homo.

E 1 (bases 1 to 461)

S Hillier,L., Allen,M., Powles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie, J., Waterston,R. and Wilson,R.

Washu-Marck EST project 1997

NL Washu-Marck EST project 1997

NL Ophablished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Insert Length: 875 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T., Waterston,R. and Wilson,R. washU-Merck EST Project 1997 Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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        est@watson.wustl.edu
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/db_xref="GDB:5563479"
/db_xref="taxon:9606"
/clone="IMAGE:669512"
/clone_lib="Soares_NHHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart,
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Matches 21
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                                                                                                                                                                                                                                                                                                  Zhang,X.

Zhang, X.

Distinct gene expression profiles of rat dorsal root ganglion induced by peripheral nerve axotomy

Unpublished (2001)
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DRABNG04 Rat DRG Library
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Xiao, H.S., Han, Z.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG666575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 446.
                                                                                            This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Pudong New Area, P.R.China. Please contact with Zhang Xu
                                                                                                                                                                                                                                                             Contact: Zhang Xu
Laboratory of Sens
                       BACKWARD: T7
                                                            PCR PRimers
                                                                                                                                                            Email: xu.zhang@ion.ac.cn
                                                                                                                                                                               Fax: 86-21-64713446
                                                                                                                                                                                                    320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
                                                                                                                                                                                                                                          Institute of Neuroscience
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG666575.1
Seq primer: T3
                                       FORWARD: T3
                                                                           (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                              iao,H.S., Han,Z.G., Zhang,F.X., Huang,Q.H., L
Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_12: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanccyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.B. clones 260232-265223, 340488-345479, and 484488-489479."
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pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:6044159"
/db_xref="taxon:9606"
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100.0%; Pr
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0; Mismatches
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Rattus
                                                                                            Shoujing Road, Zhangjiang Hi-Tech
Please contact with Zhang Xu
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R., Li,N.G.,
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; Murinae;
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ne DRABNG04 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG573124 488 DP IIIKNA IIIICUI --- 602594129F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4721382 5',
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 488)
                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LICM1577 row: j column:
                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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              ۵
              Library.
a 88
                                     /clone="IMAGE:4721382"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (TI phage-resistant)"
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116 c 125 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Rat DRG Library"
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Pred. No.
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              156
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1.4;
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AW464549
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403 TAAAGACCTTGCAAGAAAAGA 423
                                     111 TAAAGACCTTGCAAGAAAAGA 131
                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 217 333 5998
Fax: 217 244 5617
Email: h-Lewinguiuc.edu
Email: h-Lewinguiuc.edu
Email: h-Lewinguiuc.edu
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
FORWARD: TANTACGACTCACTATAGG
BACKWARD: ATTAACCCCTCACTATAGG
BACKWARD: ATTAACCCTCACTATAGG
BACKWARD: ATTAACCCCTCACTATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 489 Std Error: 0.00 Plate: BP230016A10 F. E COlumn: 9 Seg primer: AGCGGATAACAATTTCACACAGGA High quality sequence stop: 489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW464549 489 bp mRNA linear EST 24-FEB-
BP230016A10E9 Soares normalized bovine placenta Bos taurus cDNA
clone BP230016A10E9 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.

1 (bases I to 48)
Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine ESTs
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
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                                                                                                                                                                                                                         /note—"Organ: placenta; Vector: pT7T3Pac; Site_1: ECORI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "

a. B. (1997), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                                                                                  /clone="BP230016A10E9"
/clone=lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                           13.7%; Score 21; DB 9; 100.0%; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
HCGP http://www.ludwig.org.br/ORESTES.
The FARESF/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                        AW579514
MRO-HT0164-070100-013-f05 HT0164 Homo sapiens cDNA,
AW579514
                                                                                                                                                                                                                                 AW579514.1 GI:7254563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE198540 492 bp mRNA linear EST 26-JUN-2000 ug/19905.yl Soares_mammary_fland_NMLMG Mus musculus cDNA clone IMAGE:1548632 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop:
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
                                                                                                                                                                                         Homo sapiens
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/lab_host="DH10B"
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/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
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Best Local
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=MRO&t2=MRO-HTO164-
070100-013-f05&t3=2000-01-07&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0256 row: B column: 07
Seg primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                              POLYA=Yes
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                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:K0256B07-3"
/db_xref="taxon:10090"
/clone="K0256B07"
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/clone_lib="HT0164"
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/db_xref="taxon:9606"
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/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
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100.0%; Pr
'"a 0;
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Pred. No.
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FEATURES
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AI412929/c
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Best Local :
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                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp. Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST241229 Normalized rat kidney, RKIEG55 3' end, mRNA common-
                                                                                                                                                                                                                      Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI412929
AI412929.1 GI:4256433
                                                                                                                                                                                        9712, Medical Center Drive, Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                               Rat
                                                                                                                                                                                                                                                                                                           Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                    Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                               Gene
                                                                                                                                                                                                                                                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                           Genome Project:
                                                                                                                                      primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173
                                                                                                                                                                                                                                                                               Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus sp."
/db_xref="taxon:10118"
/db_one="RKIEG55"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNAs were amplified by long range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with Sali and NotI enzymes and cloned into Sali/NotI site of psPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitro
                                                                                                                   Location/Qualifiers
                                                                                                        . 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%;
100.0%;
                                                                                                                                                                                                                                                                                               Generation
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
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                                                                                                                                                                                                           Rockville,
                                                                                                                                                                                                                                                                                         of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bento Soares Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                           MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA clone
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BASE COUNT ORIGIN

200 a

140 c

105 g

144 t

Matches Query Match Best Local :

Local

Similarity 100.0%; 21; Conservative

0;

Mismatches

13.7%;

Score 21; Pred. No.

DB 9; Length 589; 1.4; 0; Indels

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DEFINITION
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AW993220
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                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                               Matches 21;
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                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=at2=RC2-BN0033-180
200-014-f04at3-2000-02-18c44-1)
Seq_primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 594)
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 bp mRNA linear
RC2-BN0033-180200-014-f04 BN0033 Homo sapiens cDNA,
AW993220
AW993220.1 GI:8253368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     Similarity
                                                                                                                                                                                       179 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence start: 20 quality sequence stop: 593. Location/Qualifiers
                                               Conservative
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                                                                                                                                                                                 /note="Organ: breast_normal, Vector: puc18; Site_1: SnaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0033"
                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Adult"
                                                                  13.7%; Score 21; DB 9; Length 594; 100.0%; Pred. No. 1.4;
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                                            Mismatches
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Search completed: August Job time: 30155 sec

2, 2002, 22:41:40

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Best Local :
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417 TAAAGACCTTGCAAGAAAAGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lnage.llnl.gov
Plate: LLAM9211 row: o column: 16
High quality sequence stop: 585.
1.597
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 597)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF169086.1 GI:11049438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:3994215"
/clone=lib="NCI_CGAP_Lu29"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic tumor, meta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                          13.7%; Score 21; DB 10; Length 597; 100.0%; Pred. No. 1.4; tive 0; Mismatches 0; Indels
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9b_ov:D14316

9b_htg:AC01985

9b_ht:AC007765

9b_ln:AC002187

9b_ln:AC002187

9b_pt:AX333515

9b_pr:AF006514

9b_pr:AF006514

9b_pr:AF00613394

9b_pr:AF0613394

9b_ov:AF181824

9b_ov:AF181827

9b_ov:AF181828

9b_ov:AF181828

9b_ov:AF181828

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database: GenEmbl:*
Database sequences: 1797656
Database length: 1873333701
Search time (sec): 4908.870000
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Query: US-08-973-363-6
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1311 I AR099026 Sequence 3 from patent
1821 I AF0644 Kommonce 3 from Datent
                                                                                                   1316 | A58696 Sequence 10 from Patent 6608 | A58691 Sequence 10 from Patent 6872 | AF004397 Gallus gallus chromo-1311 | AR0029026 Sequence 3 from Patent 153 | A58684 Sequence 3 from Patent William | A58685 Sequence 4 from Patent Wilson | A58686 Sequence 5 from Patent Wilson | A6001765 Drosophila melanogas 16420 | A6001765 Drosophila melanogas 16420 | A6001787 Dro
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5349 ! L10410 Mouse DNA-binding prote
153 ! A55683 Sequence 2 from Patent W
154 ! AF006513 Homo sapisans chrome
1 i AC074383 Homo sapiens chromd
8 i AC013394 Homo sapiens chromd
1 AF181824 Aegolius funereus chr
1 AF181825 Aegolius funereus chr
2 AF181827 Nymphicus hollandicus
2 AF181828 Nymphicus hollandicus
2 AF181828 Nymphicus hollandicus
2 AF181826 Gallus gallus chromos
2 AC07903 Homo sapiens 12 BAC
3 i AC079625 Homo sapiens chromd
4 i AC079625 Homo sapiens chromd
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KEYWORDS
SOURCE
ORGANISM
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FEATURES
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LOCUS MUSCHD1X
DEFINITION Mouse DNA-bir
ACCESSION L10410 x66028
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Location/Qualifiers
1. 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse DNA-binding protein (CHD-1) mRNA, complete cds. L10410 X66028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and sNr2/SW12-like helicase domain
Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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                                                                                                                                                                                                                                           DDEDYDNIKKSSRQATYWYSTKEDEEMKTDSDLLEVGGEDVEQPEDERETTERW
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SYEEDILERAKKKWVLDHLYJORNDTTGSTVARGTUNGAGAFSSTPPRKEELSALLKRAAE
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ELEPERNSKNWEEIIPEEQRRRLEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
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SDSESEEERDKSSCDGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
                                                  DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEF
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j M38536 Paramectum aurelia i

6 i AF2021365 Turbatrix aceti 18

2 i AX027892 Sequence 20 from P

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64 i AX083550 Sequence 15 from
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alignment_scores:
Quality: 34.00
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Percent Similarity: 100.000
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ACCESSION
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US-08-973-363-6 x A58683
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TITLE
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Sequence 2 from Patent WO9639505.
A58683
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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GLGKTIQTISTLNYLEHBHQLKGPFLLVVPLSTLTSWQRETQTWASQMNAVVYLGDIN
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BCFFILLSTRAGGLGINLASADTYVIFDSDWHPQNDLQAQARAHRIGGKKQVNIYRLVT
KGSVEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSAPSSTPFNKEELSAILKFG
AEELFKEPGBEGEFQEMDIDELIKRAETHENEBGPLTVGDELLSQFKVANFSNMDED
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KKQQQQQQQHQASSNSGSESDSSSSESDSDDSSSEV RKKKKNEDMQMSGSGSPSQS
GSDSSESEBERSSCOETESDY EPK NKVKSRK PQNRSKSKNGKKILGQKKRQIDSSE
DDDEEDYDNDKRSSRQATVNVSY KEDEEMKTDSDDLLEVCGEDVPQPEEEEFETIER
FMDCRIGRKGATGATTT IY A VEADGDPHAGF EKNKE PGEIQYLKWKGMSHIHNTWET
EETLKQQNVRGMKKLDNYKKKDOETKRWLKNASPEDVBY YNCQQELTDDLHKOY QIVE
RIIAHSNQKSAAGYPDYYCKWQGLPY SECSWEDGALISKKFQACIDEY PSRNQSKTTP
                                                                      KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
                                                    RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT
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EALSGAGSSKRRKARAKKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 cione RP11-58M12, comple
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Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
                                                                                                                                                                                                                                                                                                                                                                                       Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOB Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 134365)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .134365
                                                                                                                                                                                                                                                                                  Length: 32
Gaps: 0
Percent Identity: 100.000
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Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26882 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 26837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLys 32
                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
(bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                           Direct Submission
Submitted (21-7UL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence. AC012624
AC012624.6 GI:14993679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
/organisme"Homo sapiens"
/db_xref="taxon:9806"
/chromosome="5"
/clone="crb-2082I17"
40414 a 24497 c 25503 g 43951 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134365 bp
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JOURNAL
REFERENCE
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Magodonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Vo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACO21449 143079 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, clone RP11-58M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC021449.3
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                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 143079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 143079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 134743 bases at least Q40 Consensus quality: 139227 bases at least Q30 Consensus quality: 140814 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name:
                                                                               38821 38920:
38921 404:
                                         40412 40511:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
120: gap of 100 bp
40411: contig of 1491 bp in length
511: gap of 100 bp
43279: contig of 2768 bp in length
                                                                                                                                      38820: contig of 38820 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L5154
                                                                                                                                                                                                               the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG 10-SEP-2000
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US-08-973-363-6 x AC021449
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Quality:
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ORIGIN
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                                                                                                                                   seq_documentation_block:
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                                                                                                                                                                                                        gb_htg:AC008531
                                                                        Homo sapiens chromosome
             AC008531
                                      ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43971
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47006 5183
51831 51930:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:SP6
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17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLys 32
                                                                                                             CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 116242
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92617 106409: contig of 13793 bp in length
106410 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51831 51930: gap of 100 bp 1 169th 62620 62719: gap of 10689 bp in length 62720 75408: contig of 12689 bp in length 75409 75508: gap of 100 bp 75508: gap of 100 bp 75508: gap of 17008 bp in length 75509 92516: contig of 17008 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"assembly_fragment"
92617. 106409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
51931    62619
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47006. 51830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment" 62720. .75408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
43380. .46905
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/db_xref="taxon:9606"
/clone="RP11-58M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
106510. .143079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 100.000
145659 bp DNA 1
ne 5 clone CTC-480B11,
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                                                                                                                                                                                                                                                          to: 143079
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      906 others
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0
                 linear
WORKING
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HTG 14-FEB-2001
DRAFT SEQUENCE,
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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us-08-973-363-6 x AC008531
                                                                                                alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                  Quality: 32.00
Ratio: 1.000
Percent Similarity: 100.000
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 142744 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Outlity coverage: 6.27 in 020 bases; pulse field gel estimation
Quality coverage: 6.4 in 020 bases; pulse field gel estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs caps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 100875 100874: contig of 56174 bp in length
* 100875 100874: contig of 44600 bp in length
* 11328 118190: contig of 1008 bp in length
* 11328 118190: contig of 1008 bp in length
* 11328 118291 119694: contig of 1404 bp in length
* 113291 119694: contig of 3503 bp in length
* 113298 123397: gap of unknown length
* 113298 12397: contig of 3503 bp in length
* 113298 12397: contig of 3503 bp in length
* 113298 12397: contig of 3503 bp in length
* 113298 12397: contig of 3503 bp in length
* 113298 12397: contig of 3503 bp in length
* 113598 12397: contig of 3503 bp in length
* 123298 12397: contig of 2260 bp in length
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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DDE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .145659
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                                                            Length: 32
Gaps: 0
Percent Identity: 100.000
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seq_name: gb_htg:AC091946
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Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
4 NOTE: This is a 'working draft' sequence. It currently
5 consists of 33 contigs. The true order of the pieces
5 is not known and their order in this sequence record is
5 arbitrary, Gaps between the contigs are represented as
5 runs of N, but the exact sizes of the gaps are unknown.
5 This record will be updated with the finished sequence
6 as soon as it is available and the accession number will
7 be preserved.
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Homo sapiens chromosome 5 clone RP11-36012,
PROGRESS ***, 33 unordered pieces.
AC091946
AC091946.1 GI:14333882
HTG: HTGS_PHASE1.
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Center Project Name: 544799
Center clone name: RPCI-11_36012
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Center Code: JGI
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2668
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7495
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9197
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0: gap of unknown length
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, *** SEQUENCING IN
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of 2051 unknown of 1670

length length

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alignment_block:
US-08-973-363-6 x AC091946
                                                                                                                  alignment_scores:
Quality:
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ORIGIN
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                                                                                           Quality: 32.00
Ratio: 1.000
Percent Similarity: 100.000
                                        Align seg 1/1 to:
  87658
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141644: gap of 1
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45763:
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ig of 6151 bp in length
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g of 9903 bp in le
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                              seq_name: gb_pr:AC022121
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US-08-973-363-6 x AC026778/rev
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Quality:
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LOCUS AC026778
seq_documentation_block:
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                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                      CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 29637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Porive, Walnut Creek, CA 94598, USA On Jun 1, 2001 this sequence version replaced gi:13677045. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-MAR-2000) production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 (Dases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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WI-13675 G23101
SHGC-58345 G38487
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DOE Joint Genome Institute.
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1. .195433
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US-08-973-363-6 x AC022121/rev
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       LOCUS AC092382 276181 bp DNA linear HTG 03-JUL-2001 DEFINITION Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE,
                                                                                                                               seq_name: gb_htg:AC092382
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AC022121 from: 1 to: 219258
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                                                                                                                                                                                              89400 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 89355
                                                                                                                                                                                                                                                                                                                  89450 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 89401
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                                                                                                                                                                                                                                                                                                                                               1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu ouality: Phrap Quality >-40 99.8% of Sequence; Estimated Total Number of Errors is 0.4.
STS Content:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced g1:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHGC-58345 G38487
SHGC-103595 G57841.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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DDE Joint Genome Institute and Stanford Human Genome Center.
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AC022121.6 GI:15375145
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DOE Joint Genome Institute.
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/db_xref "taxon:9806"
/db_come="5"
/chromosome="5"
/clone="CTD-2007H13"
a 42062 c 40933 g 64309 t
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Gaps: 0
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Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 256799 bases at least Q20
Estimated insert size: 174820; agarose pestimation
Estimated insert size: 174820; sum-of-contigs estimation
Quality coverage: 8.52 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation.
*.NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gass between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Center Code: JGI
Web site: http://www.jgi.doe.gov
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Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Submitted Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Center Project Name: 435334
Center clone name: RPCI-11_75H1
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DOE Joint Genome Institute.
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AC092382.1 GI:14589571
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1061: contig of 1061 bp in length
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2927: gap of unknown length
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5618: contig of 1300 bp in length
5718: gap of unknown length
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17083: gap of unknown length
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1728: gap of unknown length
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                                          00: gap of unknown length
1005: gap of unknown length
1905: contig of 7781 bp in length
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16005: gap of unknown length
16005: gap of unknown length
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135114: gap of unknown length
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135214: gap of unknown length
137994: gap of unknown length
157994: gap of unknown length
3 171652: gap of unknown length
3 201687: contig of 29835 bp in lengt
188 231268: contig of 29835 bp in length
269 231368: gap of unknown length
1369 276181: contig of 44813 bp in le
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/chromosome="5"
/clone="RP11-75H1"
/clone=lib="RPCI human BAC library
/s1769 c 50026 g 82854 t 4673
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US-08-973-363-6 x A58696
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    Quality:
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US-08-973-363-6
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                                                                                                                                                                                                                                                                              Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                    TCGTGCAGATTACCTCATTAAATTACTG 1215
                                                                                                             gb_pat:A58691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_pat:A58696
unidentified.
unidentified
unclassified.
                                     Sequence 10 from Patent W09639505.
A58691 A58691.1 GI:3714250
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1316)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unidentified unidentified
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Sequence 15 from Patent W09639505.
A58696
                                                                                                                                                                                                                                                                                                                                                                                                                   Other
                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 9639505-A 15 12-DEC-1996; ISIS INNOVATION (GB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                      publication AU 5906996 961224.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
205 c 308 g 30
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US-08-973-363-6 x A58691
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LOCUS AF004397
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 6872)
Criffiths,R. and Korn,R.M.
A CHD1 gene is Z chronosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF004397 mRNA linear VRT 08-OCT-15 Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 6608)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chicken.
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 BQQ, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF004397.1 GI:2501845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: WO 9639505-A 10 12-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
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1207 c 1459 g 165
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/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                                                                                   /gene=
                                                                                                                                                                                                                          /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/db_xref="GI:2501846"
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                                                                                                                                                                                   "CHD-Z"
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seq_name: gb_pat:AR029026
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Ratio: 1.000
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1 (bases 1 to 1311)
de Lange, T., Steensel, Bvan. and Bianchi, A.
Altered telomere repeat binding factor
Patent: US 5859183-A 3 12-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Sequence 3 from patent US 5859183.
                                                                                                                                                                                                                                                                                                                  AR029026.1 GI:5940999
                                                                                                                                                                             Unclassified.
                                                                                                                                                                                                                                                  Unknown.
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CKVLKQRPRFVALKKQPSYIGGHSLELRDYQLNGLNWLAHSWCKGSCLIADEWGLG
KTQTGTISFLNYL-HEHGUKYGPFLLRVPLSTLTSWGRELQTWAPGDWALVYLIGDITSRN
MIRTHEWHHPOTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGVDEAHRLKNDDSLLY
RTLIDFKSNHRLLTTGTPLONSLKELWSLLHFINPEKFSSWEDFEEHEHGKREEYGYAS
LHKEKLEPFLLRFKKDVEKSLPAKVGOILKWEMSALDKOYYKWILTENYKALSKCSKG
STSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQBALQHURSSGKLILLDKLLIRLR
ERGNRYLIFSQMVRMLDILAEYLKYRQFPFQKLDGSIKGSLKRQALDHFNAEGSSDFC
FLLSTRAGGLGILMASADTVIFDSDWAPQNDLDAQARAHRIQOKKQVNIYRLYTKGS
VEEDILEBAKKKMYLDHLYJQRWDTTGKTVLHTGSTPSSSTFPNKEELSALLKGAEE
VEEDILEBAKKKMYLDHLYJQRWDTTGKTVLHTGSTPSSSTFPNKEELSALLKGAEE
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SAFSNGKDHRWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGRIKDSRGHBDHRSH
SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
HRSPFEHSSDHKSTPEHTWSSRKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="short insert found in longer variant mRNA of CHD-Z"
1 1223 c 1520 g 1683 t
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LEPERNSRMEEIIPESGARRIEBEERGKELEEIWLERMENG-KAGISFNGSEGRRSR
SRRYSGSDSDSTIERKRPXKRGFRFITERENIKGFSDAEIRRIKKFKGFLERLD
AVARDAELDENSETDLRRLGELVHURGCIKALIDNSSGGRSGRERFIKSTKKFKGFTFRISGV
QVANKLYISHDESELAPLHKGISTSHPURGEKRYVIPOHKAAHFDIGHKKENDSNULVGI
YEKYGSSMEMIKMDEDLSTYKTIPDDEKKRYVIPOHFRAAHFDIGHEKDSNULVGI
YEKYGSSMEMIKMDEDLSTYKTIPDDEKKPQAKGLGFBNYLIKLINGLARREAG
RLAGNSKKRRTRNKKNKMKASKIKBEIKSDSSGPESKSNEDDEEDNKDEIVSVK
HLHKKIKTEKBNEEKEPDIGIKKBAEBKRFTKEKNKRELKREKKEKEDKKELKEKD
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SQSGSSDSESGSESGSQSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
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ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CHD-Z"
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 29-SEP-1999
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BASE COUNT ORIGIN

REFERENCE AUTHORS JOURNAL FEATURES

TITLE

VERSION KEYWORDS

ACCESSION DEFINITION

SOURCE

ORGANISM

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WARN:
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Database sequences: 1736436
Database length: 858457221
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Query: US-08-973-363-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: Aug 3, 2002 7:18 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM of: US-08-973-363-6 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             search time (sec): 521.050000
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-MODEL-frame+_p2n.model -DEV-x1h
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-DB-N_Geneseq_032802_-QFMT=fastap -SUFFIX-o11p2n.rng
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-CAPOP-4.500 -GAPEXT-6.000 -GAPEXT-0.050 -XGAPOP-60.000
-XGAPEXT-60.000 -FGAPOP-6.000 -FCAPEXT-7.000 -YGAPOP-60.000
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-XGAPEXT-60.000 -DELOP-6.000 -DELEXT-7.000 -START-1
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-MATRIX-011g0 -TRANS-human40 cdi -LIST-45 -MODE-LOCAL -OUTENT-Pfs
-NORM-ext -HEAPSIZES-500 -MINLEN-0 -MAXLEN-20000000
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-USCAR-US0897363_CGM1_1.186 -NCPU-6 -ICPU-3 -LONGLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              out_format : pfs
alignment_scores:
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Ratio: 1.000
Percent Similarity: 100.000
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                                 US-08-973-363-6 x AAT42756
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from: 1

to: 153

Percent Identity: 100.000

27 G; 28 T; 0 other;

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                                                                                                 Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42758) and the great great gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.00 117.84
7.00 117.83
7.00 117.78
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7.00
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7.00 118.24
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24

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alignment_block:
                                                                                                                        alignment_scores:
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ID AAT42754 standard;
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                         Align seg 1/1
                                                 US-08-973-363-6 x AAT42754
                                                                                      Percent
                                                                                                                                                                                            The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken CHD-W gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102
                                                                                                                                                            Sequence 1316 BP;
                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9639505-A1
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IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                           chromodomain-helicase-DNA binding genes determine sex — used for sex determn, and to control sex of progeny
                                                                                               Quality:
Ratio:
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                         to: AAT42754
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                                                                                   26.00
1.000
100.000
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                                                                                                                                                                                                                                                                                                                                                                                                           В;
                                                                                                                                                            208 C;
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                         from:
                                                                                      Percent
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                          ب
                                                                                                                                                            306 G;
                                                                                   Identity:
                         ţo:
                                                                                               Length:
                                                                                                                                                            304 T;
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0
100.000
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                                                                                                                                                            other;
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 17
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seq_documentation_block:
ID AAT42751 standard; cE
XX
AAT42751;
AC AAT42751;
XX
DT 12-MAR-1997 (first e
.XX
Bird; sex determinati
KW Bird; sex determinati
KW CHD-W; chromodomain-H
XX
Gallus sp.
XX

YX

FH Key Locat
FT CDS 228.
FT CDS 228.
FT CDS 74tag
XX

XX

O5-JUN-1996, 96WO-G
XX

O6-JUN-1995; 95GB-G
XX

XX

(ISIS-) ISIS INNOVAFI
XX

PD 12-DEC-1996.
XX

XX

(ISIS-) ISIS INNOVAFI
XX

PD (15IS-) ISIS INNOVAFI
XX

PM (1SIS-) ISIS INNOVAFI
XX

XX

Claim 1; Fig 5; 76pp:
XX

The chicken CHD-W ger
CC The closely related of female development if
CC The Cho-lA (A = Avian
CC gene (see also AAF47)
CC Specific signal on hy
CC Specific signal on hy
CC Specific signal on by
C
                                                                                                                                                                                                                                                                                                          alignment_scores:
    Quality:
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                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                  Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                              Align
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = AVian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The chicken CHD-W gene (AAT42754) acting alone or in conjunction will the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-043127/04.
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                                                                                              seg 1/1 to:
1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INNOVATION LTD
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                                                                                                 AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95GB-0011439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 228..5390
                                                                                                                                                                                                                                                                                                                                                                                                                                     2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA; 6608
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                                                                                                 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                     1207 C;
                                                                                                                                                                                                                                                  Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1459
                                                                                                 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1653 T; 0 other;
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100.000
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seq_documentation_block:
ID AAV59280 standard; cDNA; 1311 BP.
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alignment_block:
US-08-973-363-6 x AAV59280
                                                                                                          alignment_scores:
                                            Quality: 25.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                           The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (RFF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4080 ATTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGAC 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding altered telomere repeat binding protein and related vectors 'transformants, hetero-dimers and antibodies, us to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV59280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9836066-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bianchi A, De Lange T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altered telomere repeat binding factor 1 gene.
                                                                                                                                                             Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTGCAGACTACCTCATTAAATTACTG 4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW59280.
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97US-0800264.
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/product= "A-TRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Steensel B;
                         Gaps: 0
Percent Identity: 100.000
  alignment_block:
US-08-973-363-6 x AAT42759
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Quality: 19.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                     Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                       Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Great tit CHD-W gene fragment.
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and are ignored in the translated amino
acid sequence given in Fig 3"
          Length: 19
Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID AAT42757 standard; DN
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AC AAT42757;
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                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromodomain-helicase-DNA binding genes determine sex - used for sex determn, and to control sex of progeny
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us-08-973-363-6 x AAT42758
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ID AAT42758 standard;
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                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT4758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                               Sequence 153 BP;
                                                                                                                                                                                                                    Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                          birds
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A; CHD-W; W chromosome; ss.
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and are ignored in the translated
acid sequence given in Fig 3"
                                                                                               56 A;
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ID ABL06443 standard; cDNA; 6240 BP.
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Ratio: 1.000
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Align seg 1/1 to: ABL06443 from: 1
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                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLG1676-ABL16011), expressed DNA sequences (ABLG1840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
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                                                                                                                                                                                                       Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
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DB; ABB62340.
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                                                                                           Percent Identity: 100.000
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US-08-973-363-6 x ABL06442
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P-PSDB; ABB62339.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002 (first entry)
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABL06442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventi useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
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                                           9 LysProGlnAlaLysGlnLeuGlnThrArgAla 19
                                                                                                                                                                                                                                                                                                                                                              Length: 11
Gaps: 0
Percent Identity: 100.000
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chronic colitis;
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PR XXX
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US-08-973-363-6 x AAK88882
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ID AAI57603 standard; cDNA; 421 BP.
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicits, Hirschisprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 421 BP; 148 A; 78 C; 127 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1198; 986pp; English.
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                                                                                                    Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
                                                                                                                       Human colorectal cancer antigen cDNA SEQ ID NO: 67
                                                                                                                                           19-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
 31-JAN-2000; 2000US-0179065
                                         02-AUG-2001.
                                                             WO200155350-A1
                                                                                 Homo sapiens.
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                     17-JAN-2001; 2001WO-US01350
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DB; AAM93109.
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Isolated polypeptide disorders related to and also for testing
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DB; AAM38625.
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2000US-0239937
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and
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treating, preventing and/or prognosing colon and rectum including colorectal c detection e.g. diagnosis -
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         colorectal cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antipreumatic; antiproliferative; cyrostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; pathological condition; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding number of colorectal cancer antigens. These are shown AAIS7547-AAIS7619 and AAM38569-AAM38641. These can be diagnosis, prevention and treatment of cancer of the comparation of the present sequence is a colorectal cancer antigen of
  Claim 1;
                                           Isolated nucleic acid used in preventing, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
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                                                                                                                                                                                                              Rosen
                                                                                                                                                                                                                                                                                                          13-MAY-1999;
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                                                                                                                    2000-679828/66.
DB; AAB56081.
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Page 858; 1065pp; English.
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                                                                                                                                                                                        Florence KA,
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                                              treating
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                                              molecule encoding reating or ameliora
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ameliorating
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                                           human secreted protein ing a medical condition
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rmat directly from WIPO
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alignment_block:
US-08-973-363-6 x AAC99822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:AAS96223
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                 Human; bone marrow; central nervous system disorder; haematopolesis; ss; peripheral nervous system disorder; myeloid cell disorder; osteoporosis; lymphoid cell disorder; osteoparthritis; bone degenerative disorder; stepperiodontal disease; cerebrovascular disorder; viral infection; cancer; bacterial infection; fungal infection; autolamune disorder; percent inflammatory disorder; cognitive disorder; depression; stomach; lniammatory disorder; tumour; colon; liver; bladder; prostate; kidney; ovary; brain; skin; bone; cartilage; tendon; ligament; nerve; tissue growth; tissue regeneration; wound; burn; incision; ulcer.
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          18-APR-2000; 2000US-0522929
                                                                   18-APR-2001; 2001WO-US12607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow tissue polynucleotide #9.
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Gaps:
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seq_documentation_block:
ID AAA/1645 standard; DNA; 2(
XX
AC AAA/1645;

XI 14-DEC-2000 (first entry)
XX
DE Human aspartate protease; neuror
XX
Aspartate protease; neuror
XX
Aspartate protease; psl 5
XX
Anizheimer's disease; psl 5
XX
PN W0200043505-A2.
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27-JUL-2000.
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Quality:
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US-08-973-363-6 x AAS96223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotides encoding bone marrow ctissue polypeptides. The sequences of the invention can be used in the Ct treatment of central nervous system disorders such as Parkinson's ct reatment of central nervous system disorders such as parkinson's ct disease, Alzheimer's disease, Huntington's disorders and amyotrophic constraints, peripheral nervous system disorders such as peripheral central solerosis, peripheral nervous system disorders such as peripheral constraints, bone degenerative disorders, periodontal constraints, such as stroke, viral infections, forgal infections, autoimmune disorders such as croit at infections, fungal infections, autoimmune disorders such as croit such as croit such as croit such as croit such as contraints, multiple sclerosis, asthma and eczema, inflammatory cd disorders such as croit's disease and nephritis, hyperproliferative colorary, kidney, brain and skin). The sequences are also useful in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration can din healing of wounds, burns, incisions and ulcers. Sequences are associated in healing of wounds, burns, incisions and ulcers. Sequences are associated in healing of wounds, burns, incisions and ulcers. Sequences conserved the properties of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides encoding bone marrow tissue polypeptides, useful for preventing, diagnosing and treating osteopathic diseases \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-2000; 2000US-0695783; 30-NOV-2000; 2000US-250583P; 26-JAN-2001; 2001US-0770160.
                                                                                                                                                     Aspartate profease; neuroprotectant; nootropic; gamma-secretase activity; amyloid precursor protein; APP; beta-amyloid; cleavage; Notch; Irel; Alzheimer's disease; psi 5; human; ds.
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ID AAK84450 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                           amyloid precursor protein (APP) to beta-amyloid, and also in cleavage of cother membrane proteins such as Notch (implicated in development of the nervous system); N'terminal signal peptides; C'terminal propeptides; generation of peptides for presentation in the context of major histocompatibility complex molecules, and cleavage of the endoplasmic reticulum stress sensor protein Irel. (I), also nucleic acid (II) that encodes it, and its inhibitors and antibodies (Ab) are used to treat or diagnose diseases that are associated with cleavage of amyloid precursor protein, especially Alzheimer's disease, aberrant breakdown of tydrophobic signal peptides, or accumulation of unfolded proteins in the endoplasmic reticulum. They can also be used to modify presentation of hydrophobic peptides by histocompatibility complex molecules, in cases of e.g. viral infection, cancer and transplant rejection. This sequence encodes the human aspartate protease psl 5 which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                         Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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08-JUN-1999;
24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel protease (I) that has two aspartate residues in a catalytically active structure. The aspartate residues are present in motifs of formulae X_1GX_2GD and X_3X_4DX_5 both present in a transmembrane region. The products of the invention have neuroprotective and nootropic activity. (I) represent the previously unidentified gamma-secretase activity that is involved in conversion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 31-32; 32pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-514726/46.
P-PSDB; AAB10556.
              cytostatic; gene therapy; vaccine; metastasis;
                                                   Human
                                                                              07-NOV-2001
                                                                                                       AAK84450;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2052 BP;
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                           Human; immune;
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                                                 immune/haematopoietic antigen genomic sequence
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99DE-1025946.
99DE-1029115.
                         haematopoietic; immune/haematopoietic antigen; cancer;
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PR 29-SEP-2000; 2000US-0236359.
PR 29-SEP-2000; 2000US-0236370.
PR 02-CCT-2000; 2000US-0237038.
PR 02-CCT-2000; 2000US-0237039.
PR 02-CCT-2000; 2000US-0237039.
PR 13-CCT-2000; 2000US-0240860.
PR 13-CCT-2000; 2000US-0241785.
PR 20-CCT-2000; 2000US-0241787.
PR 20-CCT-2000; 2000US-0241787.
PR 20-CCT-2000; 2000US-0241809.
PR 20-CCT-2000; 2000US-024677.
PR 08-NOV-2000; 2000US-0246674.
PR 08-NOV-2000; 2000US-0246674.
PR 08-NOV-2000; 2000US-0246674.
PR 08-NOV-2000; 2000US-0246674.
PR 17-NOV-2000; 2000US-0249214.
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XX PI Rosen CA, Barash SC, Ruben SM;
XX PI Rosen CA, Barash SC, Ruben SM;
XX PI Rosen CA, Barash SC, Ruben SM;
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides, PT metastasis.

XX Nucleic acids encoding human immune/hematopoietic antigen (I) control of the sequences given in AAM82170 to AAM91921. (I) have cytostatic control of the production of the production. (I) control of diseases associated with inappropriate (I) expression. For control of the activity of (I) by expressing inactive production of control of the activity of (I) by expressing inactive proteins or to control of the activity of (I) by expressing inactive proteins or to control of the activity of (I) by expressing inactive proteins or to control of the activity of (I) by expressing inactive proteins or to control of the activity of (I) by expressing inactive proteins or to control of the activity of (I) by expressing inactive proteins or to control of the proteins and polynucleotides may be used to produce the secreted (I), by inserting contein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting conteins and cancer metastases of heematopoietic delived cells. AAK64703 to AAK87694 represent immune/haematopoietic antigen genomic concers and cancer metastases of heematopoietic antigen genomic concers and the present invention. AAK5492 and AAM82169 concers and the present invention. AAK5492 and AAM82169 concers and the present invention. AAK5492 and AAM82169 concers and the present invention. AAK5490 and AAM82169 concers and the present invention. AAK5490 and AAM82169 concerns and polynucleotides may be used to present invention.
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4307 TCTAGGGATCTAGCAAAGCGAGAG 4330

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gb_est2:BP881342
gb_est1:A1085785
gb_est2:C84397
gb_est2:RM36296
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Carninci,P., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.,

No. Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

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"S., Kawal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 29, 2000 ***
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
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Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                        further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Grogenomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzaw, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. They are the computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Fax: 81-45-503-9216
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6 | B4422113 f157b02.y1 Sugano K
4 | BG994052 PMO-H70913-1250201-0
1 | BG999049 PMO-H70913-250401-0
1 | BG999049 PMO-H70913-250401-0
3 | AA427958 zw50a01.r1 Soares_t
2 | AQ266584 RPCTII-73H11.TK RPC
1 | BI447767 dah91g03.x1 NICHD X
                                                                 Research Group in Riken
Laboratory in RIKEN.
n Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
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                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                   ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-973-363-6 x BB155356
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                                                                                                                                                                                                                       ORGANISM
                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 CCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 luAlaGlnArgLeuCysGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est1:BB461065
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Ratio:
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BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                   Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 660)
Tagami, M.,
                                                                                                                                                                                                                                                                                            BB461065.2 GI:16426612
                                                                                                                                                                                                                                                                                                                     BB461065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.000
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/lab_host="DH10B"
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/clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
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  Tagawa, A., Takahashi, F., Takeda, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 c
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  Tanaka,T.,
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  Toya, T.,
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VERSION

alignment_scores:

Quality: Ratio:

41

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FEATURES
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated with 384 multicapillary sequencer. Genome Res. sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jul 21, 2000 this sequence version replaced gi:9356558 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001 On Jul 21, 2000 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki,Y
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                               211
                     was cleaved with BamHI and XhoI. Vector: a pBluescript KS(+) after bulk excision from a 130 c 168 q 151 +
                                                                                                                                                                                                                                                                                              prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                               transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D130070B13"
                                                                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
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EST 07-MAR-2000

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AUTHORS
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VERSION
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US-08-973-363-6 x BB461065
  alignment_block:
US-08-973-363-6 x AL601246
                                                                                                                             alignment_scores:
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ORIGIN
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LOCUS ALGOIDAG
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                                                          Quality: 32.00
Ratio: 1.000
Percent_Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGCTCAGAGACTTTGTGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweidy/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 bp mRNA linear EST 14-AUG-2001 DKFZp313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313J1040 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 No sl sequence available.

This clone (DKF2p313J1040) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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                                                                                                                                                                                                                       163
                                                                                                                                                                                                            /clone="DKFZp3131040"

/clone=lib="313 (synonym: hlcc2)"

/dev_stage="adult"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                        Length: 32
Gaps: 0
Percent Identity: 100.000
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ORGANISM
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    Ratio:
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US-08-973-363-6 x AI890775/rev
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LOCUS AI890775
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                                                                               Align seg 1/1 to reverse of: A1890775
                                                                                                                                                                                        Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC 329
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                       1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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1 (bases 1 to 547)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index (Dpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIB9U775 547 bp
wm95fill:Xl NCI_CGAP_Ut2 Homo sap
similar to SW:CHDL HUMAN O14646
PROTEIN 1 ; mRNA sequence.
AIB90775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llni.gov/bbrp/image/image.html
Insert Length: 1924 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
1.547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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AI890775.1 GI:5595939
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                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/lab_host="DH10B"
                                                                                                                                                                                                                  32.00
1.000
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                                                                                                                                                                                   Length: 32
Gaps: 0
Percent Identity: 100.000
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sapiens cDNA clone IMAGE:2443725 3'
546 CHROMODOMAIN-HELICASE-DNA-BINDING
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alignment_scores:
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ORGANISM
                     LOCUS BE895133
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LOCUS AU125712
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                                                                            seq_name: gb_est2:BE895133
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Ratio: 1.000
Percent Similarity: 100.000
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BE895133 1028 bp n
601436060F1 NIH_MGC_72 Homo sapiens
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AU125712
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai,T.
HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
<a*ito.K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomicsehri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics המינים Helix Research Institute
Fig. 7 Years Kisarazu, Chiba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 866)
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Location/Qualifiers
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Tel: 81-438-52-3951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pME18SFL3; mRNA from uninduced
precursor cells"
a  149 c  196 g  207 t  2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="NT2RM4002061"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Percent Identity:
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                     mRNA
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nRNA linear EST 20-OCT-2000 CDNA clone IMAGE:3921087 5',
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US-08-973-363-6 x BE895133
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                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est2:BF239967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC
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                                                                                                                                                                                                         mRNA sequence.
BF239967
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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BE895133
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
                                                                                                                 Homo sapiens
                                                                                                                                                                                      BF239967.1 GI:11153890
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Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
Technologies."
238 g 198 t
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Percent Identity:
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    Collection (MGC)
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US-08-973-363-6 x BF239967
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Quality: 27.00
Ratio: 1.000
Percent Similarity: 100.000
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                                              COMMENT
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                                  Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1. (bases 1 to 591)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
           Sanger Centre
                                                                                                                                                                                                                                                                                                                                      western clawed frog.
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Plate: LLCM1033 row: k column: 18
High quality sequence stop: 562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345
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//Clone_lib="NIH_MCC_54"
//Clone_lib="NIH_MCC_54"
//Lissue_type="from chronic myelogenous leukemia"
//Lab_host="DH10B (T1 phage-resistant)"
//Lab_host="DH10B (T1 phage-resistant)
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/db_xref="taxon:9606"
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Gaps: 0
Percent Identity: 100.000
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TNeu045e20 5',
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AUTHORS
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US-08-973-363-6 x AL659353/rev
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Ratio: 1.000
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                                                                                                                                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
Sequencing primer: PIC
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 645)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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EST.
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This sequence is from a xenopus Gene Collection (XGC) library
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/Clone_1bb"XGC-neurula"
/Clove_1ib="XGC-neurula"
/dev_stage="neurula"
/lab_host="scherichia coli DH10B"
/lab_host="scherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BCORI at the 5' end and NotI at the 3' end."
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="L1E1d12"
                                                                                                       Location/Qualifiers
1. .645
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/db_xref="taxon:8364"
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Gaps: 0
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AUTHORS
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US-08-973-363-6 x AL644594
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MEDLINE
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QV3-BN0047-150400-152-c03 BN0047
AW997058
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                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                       (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
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                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
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/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end"
a 125 c 156 g 141 t 1 others
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0047"
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LOCUS AW996787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA, \lambda AW996787
                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed sequence tags % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
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200-102-d03&t3=2000-02-23&t4=1)
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154 c 126 g 241 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
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E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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/dev_stage="Adult"

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RS Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Y., Ito, M., Kawal, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Hishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakal, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takahashi, A., Muramatsu, M. and Hayashizaki, Y. Takahashi, Y. Takanashi, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Takahashi, Y., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Takahashi, Y., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Takahashi, Y. Takahashi, Y., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Takahashi, Y. T
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Contact: Yoshihide Hayashizaki
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930033J21 3', mRNA
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Imotani, K., Ishii Hayatsu, N., Hiramoto, K., Hiraoka, T., Konno, H., Kouda, M., Matsuyama, T., Nato, K., Kawai, J., Kojima, Z., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinata, K., Shinataki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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e mouse tissues.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/cell_line="RCB-0527 Jyg-MC(B)"
g6 c 108 g 96 t
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/db_xref="taxon:10090"
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alignment_block:
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     AUTHORS
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AL286261
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahari
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URL:http://genome.gsc.riken.go.jp,
Carninci.p. Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p. Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Mr. Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
%S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                     AL286261.1 GI:8024707
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Fax: 81-45-503-9216
l (bases 1 to 856)
Roest-Crollius, H.,
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                                                   Tetraodontidae;
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/cell_line="RCB-0527 Jyg-MC(B)"
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/db_xref="taxon:10090"
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                                           Tetraodon.
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Gaps: 0
Percent Identity: 100.000
  Jaillon, O.,
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  Dasilva, C.,
Fizames, C., Fisher, C
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VERSION
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LOCUS BF881342
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US-08-973-363-6 x CNS04DVG/rev
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TITLE
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                                                                                                               1 (bases 1 to 129)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovigenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                   Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                       BF881342 129 bp PM0-ET0208-031200-001-f12 ET0208
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Boung
Bernot, A., Fizames, C., Wincker, P., Brottler, P.,
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                                                                                                  Simpson, A.J.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                  Homo sapiens
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  Contact: Simpson A.J.G.
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/note="Genoscope sequence
/note="Genoscope sequence
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alignment_scores:
Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
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US-08-973-363-6 x BF881342/rev
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source
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-ETO208-
031200-001-fl2kt3=2000-12-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence stop: 128.
Location/Qualifiers
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Fax: +55-11-2707001
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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FEATURES

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Query: US-08-973-363-7
Query length: 41
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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         6242 | LT7907 Drosophila melanogaster

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446 | AX333515 Sequence 4024 from Pat

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183658 | AF181825 Aegolius funereus chromos

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348 | AF060702 Struthio Camelus Clone
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I A58685 Sequence 4 from Patent
I A58686 Sequence 5 from Patent
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A58691 Sequence 10 from Paten
AF004397 Gallus gallus chromo
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AUTHORS
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SOURCE
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Ratio: 1.000
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A58691 A58691.1 GI:3714250
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AF063890 Rattus norvegicus
S80542 related adhesion foc
D45854 Rattus norvegicus mR
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                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF004397
AF004397.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF004397 to mRNA linear VRT 08-OC Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, compload
                                                                                                                                                                                                                                                                                    Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chicken
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
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Sequence 3 from Patent W09639505
A58684
1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                      unidentified unclassified
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ERGNNYLIFSOMVRMLDILAFYLKYNGPPFÖRLDGSIKGELRKOALDHENAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDMNPQNDLDQAQARAHRIGOKKOVNIYRLVTKGS
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LFKEPEGEEQEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNMDEDDIE
LEPERNSRNWEEIIPESQRRIEEEERQKELEEIYMLDRANKCQISRNGSEGRRSR
SRRYSGSDSJTERKRFKKRGRPFTIPRENIKTGFSDAEITRRFIKSYKKFGGPLERLO
AVARDAELVDKSETDLRKLGELVHNGCIKALKNNSSGQERAGGRLGKVKGPTFRISGV
QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDMGKEDDSNLLVGI
OVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIAGUITTIL
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MIRTHEWMHPOTKRIKENIILLTYEIILKDKS FIGGINWAF IGYDEAHRIKNDOSLLY
RTILIDFKSNHRILTIGTPLONSIKEIDWSILHFINPER FSWEDDFEEEHGKGREVGYSE
LHKELEPFILRRYKKDVEKSIPAKVEQIILRMEMSALOKQYYKWIILTRNYKALSKGSKG
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
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RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSVK
HLHKKIKTEKENEEKPEPDIGIKKEAEEKRETKEKENKRELKREKKEKEDKKELKEKD
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CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
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BASE COUNT ORIGIN

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Patent: WO 9639505-A 3 12-DEC-1996; ISIS INNOVATION (GB)

FEATURES

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US-08-973-363-7 x A58685
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US-08-973-363-7 x A58684
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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                                                                                                                                                                                                                                                                                                                                                                                                                     unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                         52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy 24
                                                                                                                                                                                  Mouse DNA-binding protein (CHD-1) mRNA, complete cds. L10410 x66028 L10410.1 GI:455014 DNA binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                           Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SW17-like helicase domain
SNF2/SW17-like helicase domain
Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
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Perry, R.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 9639505-A 5 12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unclassified.
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                                   93211972
             (bases 1 to 5349)
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1. .153
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alignment_block:
US-08-973-363-7 x MUSCHDlX
   seq_documentation_block:
LOCUS AF006513
                                                                                             seq_name: gb_pr:AF006513
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                              CCGTGCAGACTACCTCATCAAACTACTT 4103
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7701 Burho
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01 Burholme Avenue, Philadelphia, PA 19111, USA
16, 1994 this sequence version replaced gi:293322.
Location/Qualifiers
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QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSRRYSGSDSDSISEKKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERL
DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSGTERAGGRLGKVKGPTFRISG
VQVNAKLVIAHEDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSK
GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSSGKLILLDKLLIRL
RERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCKYLKQRPRRVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEMGL
GKTIQTISFLNYLFHENQLYGPFLLVVPLSTLTSWGREIQTWASGMNAVVYLGDINSR
NMIRTHEWMHPOTKRLKENILLTTYEILLKDKAREIGGLWAAFIGYDEAHEKKNDDSLL
YKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREA
QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNMDEDDI
ELEPERNSKNWEEIIPEEQRRRLEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
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SDSESEEERDKSSCDGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT"
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SQSGSSDSDSGSQSESESDTSRENKVQAKPPKVDGAEFWKSSPSILAVQRSAML
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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/db_xref="taxon:10090"
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5947 bp
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Gaps:
   mRNA
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: 0
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   PRI 27-NOV-1997
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alignment_block:

Percent Similarity: 100.000

Percent Identity:

26 0 100.000

alignment_scores:

Quality:

26.00 1.000

Ratio:

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MEDLINE
REFERENCE
AUTHORS
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ACCESSION
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BASE COUNT
ORIGIN
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TITLE
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Noodage, T., Basrai, M.A., Basevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins

Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GSDSSESEEREKSSCDETESDYEFKNKVKSRKPQNRSKSKNGKKILGQKKRQIDSSEE
DDDEEDYDNDKRSSRRQATVNVSYKEDEEMTDSDDLLEVCGEDVPQPEEEEFI IER
FMDCRIGRKGATGATTIYAVLADGDDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWET
EETIKQQNVBGMKKLDNYKKKDQETKRWLKNASPEDVEYVNCQQELFDDLHKQYQIVG
RIIAHSNQKSAAGYPDYYCKWGCLPYSBCSWEDGALISKFQACIDEYFSRNQSKTTP
FKDCXVLKQRPFTALIKKQPSYIGGHBGLELRDYQLNGLHWLAHSWCKGNSCILADEM
GLGKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDIN
SRNMIRTHEWTHHQTKRLKFNILLTTYEILLKOKAFLGKUNMAFIGVDEAHRLKNDDS
LLYKTLIDFKSNHRLLITGTPLQNSLKELMSLHFINPEKFSSWEDFEEBHGKGREYG
YASJLKELEPFLLRYVKDVEKSLPAKVEQILENBGLALGKQYYYKWILTTRNYKALSKG
SKGSTSGFLMIMMELKKCCNHCYLIKPPDNNEEYNKQEALGKQYYKWILTTRNYKALSKG
                                  ø
                                  RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
RASSGGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT"
1 1004 c 1243 g 1570 t
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DFCFLLSTRAGGIGINLASADTVVIFDSDWNPONDLOAQARAREIGQKKQVNIYRLVT
KGSVEEDILERAKKKYNLDHLVIQRMOTTGKTVLHTGSAPSSSTPFNKEELSALLKFG
AEELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLTVGDELLSQFKVANFSNMDED
DIELEFERNSKNWEEIIPEDQRRRLEEEEROKELEEITMLPRWHNCAKQISFNOSEGR
RSRRSVSGSDSDSISBOKRPKKGREPRTIPENNIKGFSDAEIRRFIKSYKKFGGPLE
RLDAIARDAELVDKSETDLRRLGELVHNGCIKALKDSSSGTERTGGRLGKVKGFGFPE
                                                                                                                                                                                                  ERSKKSSYSDAPVHITASGEPVPISEESEELDQKTFSICKERMRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
                                                                                                                                                                                                                                                                                              SGVQVNAKLVISHEEELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLL
IGIYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKK
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SQSGSSDSDSGSESGSQSESESDTSRENKVQAKPPKVDGAEFWKSSPSILAVQRSAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CHD1"
164. .5293
                                                                                                                                 YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
                                                                                                                                                                      KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
                                                                                                                                                                                                                                                                  EALSGAGSSKRRKARAKKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAB87381.1"
/db_xref="GI:2645429"
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/product="CHD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CHD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="5q15-21;
l. .5947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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PRI 21-JUL-2001

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alignment_block:
US-08-973-363-7 x AC092372/rev
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LOCUS AC092372
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                                                                                                                                                                                                                                                                  Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                     Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
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                                              4075 CCGTGCAGACTACCTCATCAAATTACTT 4102
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  17 rArgAlaAspTyrLeuIleLysLeuLeu 26
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Sequencing Facility, DOE Joint Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 101220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu www-shgc.stanford.edu Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.

MOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AcO12624. The number of bases overlapped is 90404.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-58M12"
34122 a 18862 c 17827 g 30409 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                                 ACCESSION
VERSION
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AUTHORS
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AUTHORS
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US-08-973-363-7 x AC012624
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ORIGIN
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LOCUS AC021449
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LOCUS AC012624
DEFINITION Homo sapiens
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                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                        118297 CCGTGCAGACTACCTCATCAAATTACTT 118324
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Direct Submission

Submitted (21-7UL-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Jul 21, 2001 this sequence version replaced gi:14277267.

Location/Qualifiers

1. 134365
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Homo sapiens chromosome 5 clone
AC012624
AC012624.6 GI:14993679
HTG.
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
human.
                                                                                                                        AC021449 143079 bp DNA linear HTG 10-SEP-2000 Homo sapiens clone RP11:58M12, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                              AC021449
AC021449.3 GI:10047806
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Mammalla; Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
                          HTG; HTGS_PHASE1; HTGS_DRAFT.
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1.000
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/db_xref="taxon:9606"
/chromosome="5"
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24497 c 25503 g 43951 t
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Gaps: 0
Percent Identity: 100.000
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clone CTD-2082I17, complete sequence
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REFERENCE AUTHORS TITLE

REFERENCE

AUTHORS JOURNAL SOURCE

ORGANISM

KEYWORDS VERSION DEFINITION ACCESSION

REFERENCE AUTHORS

JOURNAL

COMMENT

JOURNAL TITLE

BASE COUNT ORIGIN

FEATURES

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DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A., and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham, I
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda, I
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 143079)
Birren,B., Linton,L., Nusbaum,C.
Homo sapiens, clone RP11-58M12
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Due; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved
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Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                          1 38820: contig of 38820 bp in length

38821 38920: gap of 100 bp

38921 40411: contig of 1491 bp in length

40412 40511: gap of 100 bp

40512 43279: contig of 2768 bp in length

43280 43379: gap of 100 bp

43380 45905: contig of 3526 bp in length
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                                                                                                  51831 51930:
                                                                                                                                                                  46906 47005:
62719: gap of
75408: contig
005: gap of 100 bp 51830: contig of 4825 bp in length 930: gap of 100 bp 62619: contig of 10689 bp in length 719: gap of 100 bp 75408: contig of 12689 bp in length
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Barna,N., Beckerly,R., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Lander, E
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ORIGIN
   REFERENCE
AUTHORS
                                                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                                                                                                            ACCESSION
VERSION
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alignment_block:
US-08-973-363-7 x AC021449
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                                                                                                                                                                                                                                                                                     CCGTGCAGACTACCTCATCAAATTACTT 116224
                                                                                                                                                                                                                                                gb_htg:AC008531
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                            Homo sapiens chromosome 5 clone
                                                                     Homo sapiens
                                                                                                        HTG; HTGS_PHASE2;
                                                                                                                                             AC008531
                                                                                                                                                          7 ordered pieces.
                                                                                      numan.
                                                                                                                         AC008531.3 GI:12830078
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92617 106409: contig of 13793 bp in length
106410 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length
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75509 92516: contig of 17008 bp in
92517 92616: gap of 100 bp
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62720. .75408
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92617. .106409
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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26246 c 26678 g
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REFERENCE
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US-08-973-363-7 x AC008531
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ORIGIN
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Ratio: 1.000
Percent Similarity: 100.000
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JOURNAL
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                                                         source
17 rArgAlaAspTyrLeuIleLysLeuLeu 26
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Consensus quality: 14255 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in 020 bases; sum-of-contigs estimation
Quality coverage: 6.4 in 020 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * by the finished sequence as soon as it is available the accession number will be preserved.

* 1 56174 by in length 56274: contig of 56174 by in length 56175 56274: gap of unknown length 56275 100974: gap of unknown length 100875 101974: gap of unknown length 113128 11327: contig of 12153 bp in length 113128 113279: gap of unknown length 113128 113290: contig of 4963 bp in length 118191 118290: gap of unknown length 118290: gap of unknown length 118290: gap of unknown length 118290: 119694: contig of 1404 bp in length 119695 119794: gap of unknown length 113298 123297: gap of unknown length 113298 123297: contig of 3503 bp in length 113298 123297: ontig of 32262 bp in length.
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                        Length: 26
Gaps: 0
Percent Identity: 100.000
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AUTHORS
TITLE
JOURNAL
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LOCUS AC091946
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Consensus quality: 180259 bases at least 030
Consensus quality: 180259 bases at least 020
Consensus quality: 184175 bases at least 020
Consensus quality: 184175 bases at least 020
Consensus quality: 184175 bases at least 020
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in 020 bases; agarose-fp estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the places
* is not known and their order in this sequence record is
* abbitrary Case between the Contigs are processed.
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Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING
PROGRESS ***, 33 unordered pieces.
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* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center Code: JGI
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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AC091946.1 GI:14333882
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Joint Genome Institute.
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1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
                                                  gap of unknown length
contig of 2100 bp in length
gap of unknown length
contig of 2051 bp in length
gap of unknown length
contig of 1670 bp in length
gap of unknown length
contig of 1670 bp in length
gap of unknown length
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contig of 1997 by in le
contig of 1474 bp in le
gap of unknown length
contig of 1502 bp in le
contig of 1502 bp in le
gap of unknown length
contig of 1504 bp in le
contig of 1064 bp in le
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                                                        rArgAlaAspTyrLeuIleLysLeuLeu 26
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                                     CCGTGCAGACTACCTCATCAAATTACTT
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87511: contig 6
87511: gap of 1
92791: contig 6
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92891: gap of 1
102794: contig 6
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193446: contig
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ig of 5514 bp in length
if unknown length
ig of 10422 bp in length
ig of 6151 bp in length
ig of 6151 bp in length
if unknown length
of unknown length
of unknown length
if unknown length
if unknown length
ig of 7616 bp in length
ig of 5180 bp in length
ig of 903 bp in length
if unknown length
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KEYWORDS
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                                                                                    seq_documentation_block:
LOCUS AC022121
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US-08-973-363-7 x AC026778/rev
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Quality:
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LOCUS AC026778
                                                 ACCESSION
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                                                                                                                                                                                                                                                29732 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC
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STS Content:
WI-13675 G23101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 1, 2001 this sequence version replaced gi:13677045. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2000 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 19543)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; C
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DOE Joint Genome Institute and
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SHGC-103595 G57841.
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1. .195433
                                  GI:15375145
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we 5 clone CTC-428II1, complete sequence.
                                                                                    219258 bp
                                                                    clone CTD-2007H13,
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ORGANISM

Homo sapiens

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89400 CCGTGCAGACTACCTCATCAAATTACTT 89373
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                      17 rArgAlaAspTyrLeuIleLysLeuLeu 26
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Direct Submission

Drive, Walnut Creek, CA 94598, USA

CE 4 (bases 1 to 219258)

DDE Joint Genome Institute, 2800 Mitchell

RS DDE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

AL Submitted (30-AUG-2001) DDE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Aug 30, 2001 this sequence version replaced gi:15148108.

Draft Sequence Produced by DDE Joint Genome Institute

WWW-591.doe.gov

Finishing Completed at Stanford Human Genome Center

WWW-sigc.stanford.edu

Ouality: Phrap Quality >-40 99.8% of Sequence;

Estimated Total Number of Errors is 0.4.

STS Content:

WI-5811 G04974

WI-18675 G23101
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 21928)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Sequence Sequence | Strd Orlg | ZSCOTE | ESCOTE | Len | Documentation | Sidual/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42754 | 41. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42751 | 41. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42751 | 41. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42758 | 34. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42758 | 34. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42758 | 19. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756 | 19. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAU59380 | 25. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAU59380 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU59321 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU59321 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU59321 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU59332 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU5933 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU5933 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAU5933 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA19380.DAT:AAU71800 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA19380.DAT:AAU71800 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAU60839 | 10. | SIDS1/goddata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAU33693 | 10. | SIDS1/goddata/hold-geneseq/ge
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-Q-/Cgp2_1/USPTO_Spool/US08973363/runat_01082002_080123_19849/app_query.fasta_1.638
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-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 521.050000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
Query: US-08-973-363-7
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Length: 41
Gaps: 0
Percent Identity: 100.000

to:

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XT 12-MAR-1997 (first entry)
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XT 12-MAR-1997 (first entry)
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Chicken CHD-W gene (partial sequenc XX
Bird; sex determination; chromodoma XX
CHD-W; chromodomain-Helicase-DNA bin XX
OS Gallus sp.
XX
WO9639505-A1.
XX
VO5-JUN-1996; 96W0-GB01341.
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                                                                                                                          The chicken CHD-W gene (AAT42754) acting alone or in conjunction wit the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W and CHD-1A give located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a trial control can be used for sex determin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
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alignment_scores
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                                                                                                                                                                                                                                                         The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10·12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD^-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken CHD-1A gene
                                                                                                                                                                                                                                    Sequence 6608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffiths R,
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              1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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ATTTTACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42751
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DT 12-MAR-1997 (first entry)
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Bird; sex determination; chromodo KW CHD-1A; CHD-W; W Chromosome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex
birds – used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                         Quality:
                                                                                                                              Ratio:
                                                                                          34.00
1.000
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                                                                                Percent
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                                                                                                                                                                                                                                                                                        31 G; 24 T; 0 other;
                                                                                          Length:
Gaps:
t Identity:
                                                                                          34
0
100.000
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Align seg 1/1

to:

from:

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to: 153

x AAT42757 AAT42757

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alignment_scores:
Quality:
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   Quality: 34.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                         Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW8146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \cdots_I
misc_difference 52..81
                                                                                                 Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                  Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 CA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 ATTACTGAATAAAGACCTTGCAAGAAAGGAAAGGCACAAAGGCTTGCTGGTG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 la 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 sLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGlyA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "bases 52-81 are a repeat of bases and are ignored in the translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and are ignored in the translated amino acid sequence given in Fig 3\,^{\rm m}
Length: 34
Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID AAT42759 standard; DNA; 153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-973-363-7 x AAT42758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAT42758 from: 1 to: 153
                             Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Great tit CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 CA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTG 151
Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                 Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                Avian chromodomain helicase-DNA binding genes determine sex in
                                                                                                                                                                                                                                                                     P-PSDB; AAW08149
                                                                                                                                                                                                                                                                                    WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parus major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD-1A; CHD-W; W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 la 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 SLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGlyA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                      Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                      95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
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alignment_scores:

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seq_documentation_block:
ID AAV59280 standard; cl
XX AAV59280;
XX 14-DEC-1998 (first 6
XX AV59280;
XX 14-DEC-1998 (first 6
XX AV59280;
XX ds; human; telomere 1
KW ds; human; telomere 1
KW telomere; ageing; att
XX Homo sapiens.
OS Synthetic.
XX Synthetic.
XX 20-AUG-1998.
XX W09836066-A1.
XX 20-AUG-1998.
XX 13-FEB-1998; 98WO-1
XX 13-FEB-1998; 98WO-1
XX 13-FEB-1997; 97US-(
XX 14-FEB-1998; 98WO-1
XX 14-FEB-1998; 98WO-1
XX 15-FEB-1997; 97US-(
XX 15-FEB-1997; 97US-(
XX 16-FEB-1997; 97US-(
XX 17-FEB-1998; 98WO-1
XX 18-FEB-1997; 97US-(
XX 18-FEB-1997; 97US-(
XX 18-FEB-1997; 97US-(
XX 19-FSDB; AAW59280.
XX 19-FSDB; AAW59280.
XX Wucleic acid encoding pr related vectors - traper to inhibit shortening or telomere repeat bind CC telomere repeat bind CC hetero-dimer with TRR celatero-dimer with TRR celatero-dimer with TRR sequence.
CC Inhibit shortening op CC inhibit shortening op CC inhibit shortening op CC inhibit shortening op CC cells expression of recelateral celatero-dimer with TRR c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-973-363-7 x AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAT42759
                                                                                                                            The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-480769/41.
                                                                    tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 110-111; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACTGAATAAAGACCTTGCAAGAAAAGAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Lange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0018628.
97US-0800264.
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1.000
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1..1311
      recombinant proteins or where testing, eliminating the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA; 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent
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Identity:
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6
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0
100.000
         intended for subsequent for transformation.
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alignment_block: US-08-973-363-7 \times AAV59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _documentation_block:
Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = AvLan) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-IA (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                      Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse CHD-1 gene (bases 3855-977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1311 BP; 441 A;
                                                                                                                     Claim
                                                                                                                                                                                                WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                 05-JUN-1996;
                                                                                                                                                                                                                                                                                                                          12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHD-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT42756 standard; DNA; 153
                                                                                                                                                                                                                                              (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rArgAlaAspTyrLeuIleLysLeu
||||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGTGCAGACTACCTCATCAAACTA 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756
                                                                                                                                             chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                    8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHD-W; W chromosome;
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                                                                                                                                                                                  AAW08146
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                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                          "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257
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progeny.

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seq_documentation_block:
ID ABL06443 standard; cDNA; 6240 BP
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US-08-973-363-7 x AAT42756
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAT42756
                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL01875) and the encoded proteins (ABB57377-ABB72072).
         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 153 BP; 61 A; 37
                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                              Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                   interactions
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2000US-0614150
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seq_documentation_block:
ID ABL06442 standard; cDNA; 9933 BP.
    seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL06442
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US-08-973-363-7 x ABL06443
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                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ676-ABLJ6511), expressed DNA sequences (ABLJ684-CABLJ685) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
  Sequence 9933 BP;
                                                  (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Dosophila and for elucidating cell signalling and cell-cell interactions -
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
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                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABB62339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LysProGlnAlaLysGlnLeuGlnThrArgAla 19
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1.000
2711 A; 2468 C; 2538 G; 2216
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Gaps: 0
Percent Identity: 100.000
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    0 other
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alignment_scores:

Quality: 11.00 Ratio: 1.000

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alignment_block:
US-08-973-363-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ss.
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     2000US-0186528
2000US-0186528
2000US-0186530
2000US-0198073
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       ק, מסמים מיטים מיטים מיסים מיסים מיסים מיטים מ
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14-SEP-
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2000US-0246633.
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2000US-0246474.
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2000US-0232401
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2000US-0236370
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2000US-0229509.
2000US-0229513.
2000US-0230437.
2000US-0230438.
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2000US-0232081.
2000US-0231968.
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2000US-0231414
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2000US-0231244
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seq_documentation_block:
ID AAI57603 standard; cDNA; 421 BP.
XX AAI57603;
AC AAI57603;
XX
DT 19-OCT-2001 (first entry)
XX
DE Human colorectal cancer antigen of
                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-973-363-7 x AAK888882
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                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AA157603
                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAK88882 from: 1
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive relative colitis.
  Human colorectal cancer antigen cDNA SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1198; 986pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \frac{1}{2}
                                                                                                                                                                                                                                                146 AAGCAGCTACAGACCCGAGCGGATTACTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system antigen of the invention.
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                                                                                                                                                                                                                                                                        13 LysGlnLeuGlnThrArgAlaAspTyrLeu 22
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DB; AAM93109.
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Gaps: 0
Percent Identity: 100.000
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2000US-0241221.
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2000US-0234998
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5-0249244.

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5-0249264.

5-0249265.

5-0249297.
seq_documentation_block:
ID AAV33521 standard; cDNA; 252 BP
XX
AC AAV33521;
XX
29-DEC-1998 (first entry)
XX
Clone 23789 cDNA fragment encod
XX
Protein kinase; cell signalling
KW human X-linked agammaglobulinae
KW eartherosclerosis; glioma; reste
KW artherosclerosis; glioma; reste
KW cHKFRNK chiken tyr kinase; ss.
XX
OS Homo sapiens.
XX
OS Homo sapiens.
XX
OF-AUG-1998.
XX
PP 07-AUG-1996; 96US-0700575.
XX
PR 07-AUG-1996; 96US-0700575.
XX
PA (INCY-) INCYTE PHARM INC.
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Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
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US-08-973-363-7 x AAI57603
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAIS7547-AAIS7619 and AAM38569-AAAI38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or retries the present sequence is a colorectal cancer antigen coding sequence the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide for treating, preventing and/or disorders related to the colon and rectum including co and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein kinase; cell signalling; inflammation; carcinoma; diabetes; human X-linked agammaglobulinaemia; nonspherocytic haemolytic anaemia; artherosclerosis; glioma; restenosis; cholera-based septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
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DB; AAM38625.
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                                                              Hawkins PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from:
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Percent Identity: 100.000
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                                                              Wilde CG;
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other;

part of the printed directly from WIPO

rectum.

protein kinase

homolog.

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seq_documentation_block:
ID ABA61903 standard; DNA; 544 BP.
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US-08-973-363-7 x AAV33521
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Ratio: 1.000
Percent Similarity: 100.000
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Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
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                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00669.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-023659.
2000US-023659.
Chen W,
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    Rank DR;
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Single exon nucleic acid probes for analyzing gene expression in

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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK10214
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US-08-973-363-7 x ABA61903
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring and displaying gene expression in samples derived from fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direction wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 544 BP; 144 A; 128 C; 88 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 10208; 639pp + sequence listing; English.
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Gaps: 0
Percent Identity: 100.000
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US-08-973-363-7 x AAK10214
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  seq_documentation_block:
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                             Penn
                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 10205; 650pp + Sequence Listing; English
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                     Example 4; SEQ ID NO: 10669; 658pp + Sequence Listing; English.
                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                             WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK36112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCTGATAAAGTTATTAAATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                2001-488900/53.
                                                                                                                                                             SG,
                                                                                                                                                                                         MOLECULAR DYNAMICS INC.
                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                   2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236559
2000US-0236559
2000US-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                           Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266
                                                                                                                                                           Rank DR;
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US-08-973-363-7 x AAK36112
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
                                                        Align seg 1/1 to:
                                                                                                                                                                                                                                                     samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                          Sequence 544 BP;
243 TACCTGATAAAGTTATTAAATAAG 266
              21 TyrLeuIleLysLeuLeuAsnLys
                                                          AAK36112
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Gaps:
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gb_est1:AA305759
gb_est1:AI870450
gb_est2:H61027
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gb_est1:R0125712
gb_est2:B895133
gb_est1:R895787
gb_est1:B830730
gb_est1:B8309967
gb_est1:B8930730
gb_est1:B8930730
gb_est1:B8930967
gb_est2:R8939967
gb_est2:R89397058
gb_gss:CNS04DVG
gb_est1:R891342
gb_est1:R891342
gb_est1:R891342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database sequences: 13736207
Database length: -1841457050
Search time (sec): 4311.510000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query length: 41
Database: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Query: US-08-973-363-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:N49703
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est2:BM362956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est1:AW168274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL-frame+_P2n.model -DEV=xlh
-Q-/cgn2_1/UsPf0_spool/Us08973363/runat_01082002_080123_19814/app_query.fasta_1.638
-Q-/cgn2_1/UsPf0_spool/Us08973363/runat_01082002_080123_19814/app_query.fasta_1.638
-DB=EST -QFMF=fastap -SUFFIX-01ip2n.rst -GAPOP=4.500
-GAPEXT-0.050 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-GAPOP=4.500 -QGAPEXT-0.050 -XGAPOP=60.000 -VGAPEXT-60.000
-GAPOP=4.500 -GAPEXT-7.000 -YGAPOP=60.000 -YGAPEXT-60.000
-GELOP=6.000 -FGLEXT-7.000 -YGAPOP=60.000 -THR_SCORE-quality
-THR_MIN-1.1IST-45 -DOCALIGN-200 -THR_SCORE-quality
-THR_MIN-1.ALIGN-15 -MODE-LOCAL -OUTEMT-pfs -NORM-ext
-GUSER-US08973363_e(CG)1_1_2938 -NCCPU=6 -1CPU-3 -LONGLOG
-USUR-US0897363_e(CG)1_1_2938 -NCCPU=6 -1CPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLEXY -WAIT -THREADS-1
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3. 9e 19

9. 6e 19

9. 6e 16

1. 0e 14

1. 1e 14

2. 7e 13

4. 9e 10

0. 3e 10

0. 0648

0. 1514

0. 1514

0. 1573

0. 1573
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.7e-19
.4e-19
ALG5953 ALG59353 XGC-neurula SALG64594 ALG64594 XGC-egg Silux ALG64494 ALG644594 XGC-egg Silux ALG644594 XGC-egg Silux ALG61245 EXEX. SILUX SILU
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gb_est1:AA477885
gb_est2:BF901677
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gb_est2:H38315
gb_est1:AW354153
gb_est1:AA427958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
        seq_documentation_block:
LOCUS AL644594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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LOCUS AL659353
                                                                       seq_name: gb_est1:AL644594
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 30.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                            US-08-973-363-7 x AL659353/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                           296 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTG 257
                                                                                                                                              17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeu 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL659353.1 GI:17672995
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Huck
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence
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1 (bases 1 to 593)
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319
322
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Align seg 1/1 to reverse of: AL659353 from: 1 to: 593
                                                                                                                                                                                                                                                                                         1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Silurana tropicalis"
//db_xref="taxon:8154"
//db_xref="taxon:8154"
//clone=_lib="XGC-neurula"
//clone_lib="XGC-neurula"
//dev_stage="neurula"
//lab_host="Escherichia coli DH10B"
//note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. was oligo dT primed from 5ug of poly a+ RNA from neurula. EcoRI antoli cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

19 a 134 c 114 g 226 t
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Gaps: 0
Percent Identity: 100.000
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H83315 yp70c06.rl Soares adu
AW354153 32640 MARC 2PIG Sus
AA427958 zw50a01.rl Soares_t
HH228000 1005143E10.xl 1006
AA477885 zu34e05.rl Soares o
BF901677 PM4-MT0201-091200-0
linear
                                                                                                                                                                                                                                                                                         297
EST 07-NOV-2001
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REFERENCE
AUTHORS
TITLE
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Quality:
                                                                                                                                                                                                                    seq_name: gb_est1:AL601246
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                  REFERENCE
                                                              SOURCE
ORGANISM
                                                                                                        VERSION
                                                                                                                                                           DEFINITION
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                                                                                           KEYWORDS
                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 1.000 Percent Similarity: 100.000
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 AUTHORS
                                                                                                                                                                                                                                                                                                                506
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                                                                                                                                                                                                                                                   A30 bp mRNA DKFZp313J1040_r1 313 (synonym: hlcc2) Homo DKFZp313J1040 5', mRNA sequence. AL601246
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing primer: PIC
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger xenopus tropicalis EST project TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL644594 XGC-egg Silurana tropicalis cDNA clone L1E1d12 5', mRNA
Bloecker, H., Boecher, M.,
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                              Homo sapiens
                                                                                             EST
                                                                                                            AL601246.1 GI:15164752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              western clawed frog
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                (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="L1E1d12"
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Brandt, P.,
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Mewes, W.,
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 and Wiemann
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SOURCE
ORGANISM
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LOCUS AI890775
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US-08-973-363-7 x AL601246
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ORIGIN
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                                                                                                                                                                       TITLE
                                                                                                                                                                                           AUTHORS
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                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:AI890775
                                                                                                                                                                                                                                                                                                                                                        wm95f11.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:24437.25 3' similar to SW:CHD1_HUMAN O14646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1; mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone (DKFZp313J1040) is available at the RZPD in Ber
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
Berlin-Charlottenburg, GERMANNY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dKfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 547)
                                       Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                             AI890775.1 GI:5595939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No s1 sequence available
cDNA Library Arrayed by: Greg Lennon, Ph.D.
                      cDNA Library Preparation: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="DKFZp313J1040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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1.000
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Gaps:
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                                                             Ph.D.,
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alignment_block:
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                                                                                                                                                                                                                                          JOURNAL
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LISH MUSTUCCIUMS

EUKATYOTE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

EUKATYOTE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

CE 1 (bases 1 to 619)

RS Arakawa, T. Carninc(1,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,

Hiramoto,K., Hori,F., Ishil,Y., Ito,M., Kawai,J., Konno,H., Kouda,

M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki

D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,

Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Hayashizaki,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Hayashizaki,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 bp mRNA linear EST 18 BB155356 RIKEN full-length enriched, 16 days neonate thymumusculus cDNA clone A130024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
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Insert Length: 1924 Std Error: 0.00
Seq primer: 40DP from Giboo
Seq primer: 40DP from Giboo
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/clone_lib="moderately-differentiated endometrial
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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ORIGIN

COMMENT

TITLE

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alignment_block:
US-08-973-363-7 x BB155356
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                                                                                                                                    Quality: 26.00
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Email: genome res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci.P. Shibata, K., Hayatsu.N., Sugahara, Y., Shibata, K., Itoh

Carninci.P., Shibata, Y., Wuramatsu.M. and Hayashizaki, Y.

.M. Konno, H., Okazaki, Y., Muramatsu.M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi.K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashiyaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,V., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashiasi
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                                                                         194 a
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DHIOB"
/note="sit-"
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/clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
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/dev_stage="16 days no
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SOURCE
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muzamatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jappel: 81-45-503-9222
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinayawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONDO, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Jul 21, 2000 this sequence version replaced g1:9356558
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Arakawa, T., Carninci, P., Fukuda, S.,
                                                                 Encyclopedia Project of Genome Exploration Research Group in RIGEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed t
                                                   prepare mouse tissues
                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                   ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                      Location/Qualifiers
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                                                                                                                             Research Group in Riken
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US-08-973-363-7
                                                                                                                                                             COMMENT
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531 CCGTGCAGACTACCTCATCAAACTACTT 558
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                                                                                                                            Isogai,T.
HRI human CDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 866)
                                                                                                                                                                                                                                                                                                                                                                                                     AU125712.1 GI:10950428 EST.
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU125712 NT2RM4 Homo sapiens cDNA clone NT2RM4002061
                                                                Helix Research Institute
                                                                                                                                                                                                                                                                    Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
                                                                                         Genomics Laboratory
                                                                                                                                                                                                                                             Nakamura,Y., Nishikawa,T.,
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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/dev_stage="12 days embryo"
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/db_xref="taxon:10090"
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                                         Kisarazu,
                                                                                                              Isogai
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                                                                                                                                                                 wa,M., Ishii,S.
Nagai,T., Suzu
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US-08-973-363-7 x AU125712
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                        Plate: LLAM9753 row: h column: 16 High quality sequence stop: 488.
                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammallan Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1028)
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                                                                                                                                                                                                                                                                                                                     ODNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Library Arrayed by: The formation of the Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can be
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/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"
312 a 149 c 106 ~ ~~
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:39211087"
/clone_lib="NIH_MGC_72"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_bost="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stor: 37
High quality sequence stop: 337.
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW996787 37 bp mRNA linear EST 05-JUN-200
QV3-EN0047-230200-102-d03 BN0047 Homo sapiens cDNA, mRNA sequence.
AW996787
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Average insert size 2 kb. Library co
Technologies."
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESPES CR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
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                                                                                                               /clone_lib="BN0047"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Inotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB830730 RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA Mus musculus cDNA clone G930013K04 3', mRNA
                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 59 c 72 g 123 t
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Gaps:
Percent Identity:
Shibata, K., Itoh, M., Carninci, P., Sugahara
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BASE COUNT
ORIGIN
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ORGANISM
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LOCUS BB834922
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US-08-973-363-7 x BB830730
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                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                       Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Skomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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BB834922
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Computer-based methods for the mouse full-length cDNA

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                      Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                             Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                      2001
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Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
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                                                                                                          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                    Laboratory for Genome Exploration Research Group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
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/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
1 96 c 108 g 96 t
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/db_xref="taxon:10090"
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alignment_block:
US-08-973-363-7 x BB834922
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LOCUS BF239967
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Ratio: 1.000
Percent Similarity: 100.000
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                                                NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gappbs-remail.nih.gov
Tissue Procurement: ATCC
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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CDNA Library Preparation: CLONETECH Laboratories, Inc CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L
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1. .446
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/db_xref="taxon:10090"
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AUTHORS
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FEATURES

BASE COUNT

REFERENCE AUTHORS

VERSION

ACCESSION KEYWORDS

SOURCE ORGANISM

DEFINITION

COMMENT

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alignment_block:
US-08-973-363-7 x BF239967
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LOCUS AW997058
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                          TITLE
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Dias Netco, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Rocidman, G.H., Carvalho, A.F., Matsukuma, A., Balia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.Y., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Contact: Simpson A.J.G.
Laboratory of Cancer Genetic
Ludwig Institute for Cancer
                                                                                                                                                                                                                                                Simpson, \boldsymbol{A},\boldsymbol{J}. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QV3-BN0047-150400-152-c03 BN0047 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM1033 row: k column: 18 High quality sequence stop: 562.
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM1033 row: k column: 18
                                                                                                                                                                                                                                sequence tags
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                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Gaps: 0
Percent Identity: 100.000
                                              Genetics
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ORGANISM
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Ratio:
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Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS04DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103KOB of library G from Tetraodon nigroviridis, genomic survey
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This sentry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=&t2=QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                1 (bases 1 to 856)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizames, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                              Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                           AL286261.1 GI:8024707
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High quality sequence stop: 678.
Location/Qualifiers
                                                                                                                                                 Weissenbach, J
                                                                                                                                                                                                                                           Tetraodontidae; Tetraodon.
                          Roest-Crollius, H.,
                                                                        Unpublished
                                                     (bases 1 to 856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue mRNA and cDNA amplification were performed low stringency conditions."
154 c 126 g 241 t
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  lius,H., Jaillon,O., Dasi
Fizames,C., Wincker,P.,
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Dasilva,C., Bouneau,L., Fisher,C.
P., Brottier,P., Quetier,F.,
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                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF881342.1 GI:12271468 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saurin, W. and Weissenbach, J.
Human gene number estimate provided by
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                             Fax: +55-11-2707001
                                                                  Tel: +55-11-2704922
                                                                                                              Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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                      Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                 sequence tags
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sequence was derived from the
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FAPESP/LICR Human
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  Cancer Genome
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Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMOst2=PMO-ET0208-031200-001-fl2at[s]=2000-12-03&td=1)

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High quality sequence stop: 128.
Location/Qualifiers
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Location/Qualifiers
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gb. pr: AC022121
gb. httg: AC092282
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gb. pat: ANC92283
gb. pat: ANC902183
gb. pat: ANC902184
gb. httg: AC01986
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gb. in: DROCHDIA
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-USER-US08973663_GCGN1_1_4551 -MCDU-6 -LCPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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Query: US-08-973-363-8
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19511 i AR022212 Homo Sapiens chromc
1311 i AR022928 Sequence 3 from paten
153 i AS8683 Sequence 2 from Patent
14530 i AC002765 Drosophila melanogaste
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16 : A58696 Sequence 15 from Patent

172 : A58691 Sequence 10 from Patent

172 : AF004397 Gallus gallus chromo-

183 : A58681 Sequence 3 from Patent W

184 : A58685 Sequence 4 from Patent W

185 : A58685 Sequence 5 from Patent W

186 : A58686 Sequence 5 from Patent W

187 : L10410 Mouse DNA-binding prote

187 : L10410 Mouse DNA-binding Prote

188 : AF006513 Homo Sapiens CHD1 mRN

188 : AF006513 Homo Sapiens CHD1 mRN
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LOCUS A58691
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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AR063890 Rattus norvegicus
S80542 related adhesion foc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome li
Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    дикатуота; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other
                                                                                                                                                                                                                                                                                                  Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                   Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF004397.1 GI:2501845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chicken
                                                                                                                                                                                                                                                                                                                                                                      bases 1 to 6872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       publication AU 5906996 961224.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:32644"
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128. .5654
                                                                                                                                                                                                                          /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
                                                                                      /product="chromo-helicase-DNA-binding
                                                                                                                      /note="CHD protein with hydrophilic domain"
                                                                                                                                          /gene="CHD-Z"
/function="role in chromatin architecture"
                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                         codon_start=
                                                                                                                                                                                                                                                                  .6872
                                                                                                                                                                                                              .6872
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                                                                                       Z chromosome
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alignment_block:
US-08-973-363-8 x AF004397
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                        gb_pat:A58684
                                                                                                                                                                                                                                                           153 bp
Sequence 3 from Patent W09639505.
A58684
1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                               unidentified unidentified
                                                                                             unclassified
                                                                                                                                                                                                                                   A58684.1 GI:3714247
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LHKELEPFILRRVKKUVEKSIPAKVEQILRWSLHFINDEKFSSWEDFDEEEHGKGREYGYAS
LHKELEPFILRRVKKUVEKSIPAKVEQILRWSALQKQYYKWILTRUYKALSKGSKG
STSGFINIMAEIKKCCHCYLIKPDDDEFYNKOSALQHLIRSSGKLILTKLKLIRLR
ERGRRVLIFSQMVRMLDILASYLKYRQFPFQRLDGSIKGELRKQALDHPWABGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKGS
VEEDJILERAKKKMVLDHLVIQRMDTTGKTVLHFGSTPSSSTPFNKEELSAILKFGAEE
LFKEPEGEEQEPQEMDIDEILKRAETRENEEPGPLTVGDELLSQFKVANFSNMDEDDIE
LEPERNSRNWEEIIPESQRRRIEEERQKELEEIYMLPRURNCAKQISFNGSEGRRSR
SRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKGFFRISGV
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QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDLIMGKEDDSNLLVGI
YEYGYGSWEMIKMDPDLSLTQKILPDDPDKKPQAKQLQTFAADYLIKLLNKOLARKEAQ
RLAAGANSKRKTRNKKNKKASKIKEEIKSDSSPQPSEKSDEDEEEDNKDEIVSYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="short insert found
1223 c 1520 g 1683
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
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NKEKRENKVKESTOKEKEVKEEKVNEMKSENKEKSKKIPLLDTPVHITATSEPVPISE
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MIRTHEWMHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGVDEAHRLKNDDSLLY
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CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII</u>
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CHD-Z"
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Percent Identity: 100.000
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BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE

VERSION KEYWORDS SOURCE

ORGANISM

ACCESSION DEFINITION seq_name:

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REFERENCE
AUTHORS
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SOURCE
                                                                                                     alignment_block:
US-08-973-363-8 x A58685
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US-08-973-363-8 x A58684
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LOCUS A58685
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ACCESSION
                                                                                                                                                   Quality: 34.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                   Align seg 1/1 to: A58685 from: 1 to: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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24 SLEULEUNASILYSASPLEUNLARTSUSGLUNLAGINATSLEUNLAGINAS 41
24 SLEULEUNASILYSASPLEUNLARTSUSGLUNLAGINAS 41
25 ATTACTGANTANGACCTTGCAAGAAGGAAGGACACAAAGGCTTGCTGGTG 151
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41 la 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                           Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified.
1 (bases 1 to 153)
Griffiths, R. and Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
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Sequence 4 from Patent WO9639505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 9639505-A 3 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 9639505-A 4 12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified.
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                                                                                                                                                                                                                                                                         /organism="unidentified"
/db_xref="taxon:32644"
a 36 c 31 g 30
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/db_xref="taxon:32644"
a 40 c 31 g 2/
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SOURCE
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SOURCE
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US-08-973-363-8 x A58686
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                                                                                                                                                                                                                                       ACCESSION
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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                               MEDLINE
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                                                                                                                                                                                                                                                                                                                                                         152 CA 153
                                                                                                                                                                                                                                                                                                                                                                                                                            52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA 101
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                                                                                                                                                                                                                               muschulk 5349 bp mRNA linear F
Mouse DNA-binding protein (CHD-1) mRNA, complete cds.
L10410 x66028
                                                           Mus musculus
Eukaryott; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWI2-like helicase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5 from Patent WO9639505.
A58686
                                                                                                                                                                                                 L10410.1 GI:455014
DNA binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A58686.1 GI:3714249
Perry, R.P.
                               93211972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unclassified
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                                                                                                                                                                                     house mouse.
             (bases 1 to 5349)
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                                             Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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/db_xref="taxon:32644"
34 c 31 g 28
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alignment_block:
US-08-973-363-8 x MUSCHD1X
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Quality:
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                                                                                   seq_name: gb_pr:AF006513
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REGGRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQLDHFNAEGSSDF
CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGOKKQVNIYRLVKG
SYEEDILLERAKKKMYLDHLVIQRMDTTGKTVLHTGSAPSSSTPFNKEELSAILKFGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMIRTHEWMHPOTKRLKFNILLTTYEILLKDKAFIGGLNWAFIGVDEAHRLKNDDSLL
YKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
SLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT"
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HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNMDEDDI
ELEPERNSKNWEEIIPEEQRRRLEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEDEEFETIERVM
DCRVGRKGATGATTTIYAVEADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLYKHAIKKRQESQQNSDQNSNVATTHVIRNPDMERLKENTNHDDSSRDSYSSDRHLS
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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171. .
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/db_xref="taxon:10090"
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Quality:

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TITLE
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1 (bases 1 to 5947)
Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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Woodage,T.
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GLGKTIQTISTLNYLFHEHQLYGPFLLVVPLSTLTSWORETQTWASQMNAVVYLGDIN
SRNMLRTHEWTHOFTKRLKF WILLTTYEJILKOKA FLOGLINWA ET GVDEAHRIKNDDS
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YASLHKELEPFLLRVKKCDVEKSLPAKV BOI LENEMSALOKQYYKWILTRNYKALSKG
SKGSTSGELNIAMELKKCCNHCYLI KPDDNIEFY MKQEALOHLLTSGKILLDKILLI
RLEBRONRVLLFSQWVENLDILAEYLKY RQFPFQRLDGSIKGELKKQALDHFNAEGSE
DFCFILLSTRAGGLGINLASADTYVI FDSDWHPONDLOAQARAHRIGGKKOVNI YRLVT
KGSVEEDI LERAKKKWYLDHLVIQRMDTTGKTVLHTGSAPSSTFFIKEELSAILKFG
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DIELBPERGERGEPQEMDI DEILKRAETHENEBGRLFVAGALFRNENCAKQISFNGSBGR
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RLDALARDAELVDKSETDLRRLGELVHRGCIKALKDSSGGTETTGGRLGKVKGPTERI
SGVQVNAKLVISHEBELI PLHKSIPSDPEERKOYTIPCHTKAAHFDINGKKEDDSNLL
SGVQVNAKLVISHEBELI PLHKSIPSDPEERKOYTIPCHTKAAHFDINGKEDDSNLL
SGVQVNAKLVISHEBELI PLHKSIPSDPEERKOYTIPCHTKAAHFDINGKEDDSNLL
SGVQVNAKLVISHEBELI PLHKSIPSDPEERKOYTIPCHTKAAHFDINGKEDDSNLL
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KKQQQQQQQQQHQASSNSGSEEDSSSSEDSDDSSSEVKRKKHKDEDWQMSGSGSPSQS
GSDSESEEEREKSSCDETESDYEPKNKVKSRKPQNRSKSKNGKKILGQKKRQIDSSEE
                                    RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT"
                                                                                                                                                                                 GLSEREQLEHTROCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
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FMDCRIGRKGATGATTTIYAVEADGDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWET
                                                                         RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDE
                                                                                                                                                   KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
                                                                                                                                                                                                                      ERSKKSSVSDAPVHITASGEPVPISEESEELDQKTFSICKERMRPVKAALKQLDRPEK
                                                                                                                                                                                                                                                       EALSGAGSSKRRKARAKKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EETLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVG
RIIAHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALISKKFQACIDEYFSRNQSKTTP
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/db_xref="GI:2645429"
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164. .5293
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                        [GIYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MNGHSDEESVRNSSGESSQSDDDSGSASGSGSGSSSSGSSSDGSS/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="5q15-21; near WI-5811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="5"
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US-08-973-363-8 x AF006513

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                              Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
                                                                                                                                                                                                 US-08-973-363-8 x AC092372/rev
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                                                   26932 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC 26883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4075 CCGTGCAGACTACCTCATCAAATTACTT 4102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                            1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
Estimated Total Number of the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 10120)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 101220) DOE Joint Genome Institute and Stanford Human Genome Center.
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Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-58M12"
18862 c 17827 g
                                                                                                                                                                                                                                                                        Percent Identity: 100.000
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                                                                                                                                                   seq_documentation_block:
LOCUS AC021449
                                                                                                                                                                                                                     seq_name: gb_htg:AC021449
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                                                                                                                          DEFINITION
  SOURCE
                         KEYWORDS
                                                   VERSION
                                                                         ACCESSION
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                                                                                                                                                                                                                                                                     118247 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 118296
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1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17

AC021449 DNA linear HT-Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE,

HTG 10-SEP-2000 CE, 10 unordered

AC021449 AC021449.3 GI:10047806 HTG; HTGS_PHASE1; HTGS_DRAFT.

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REFERENCE
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alignment_block:
US-08-973-363-8 x AC012624
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                                                                                                                              alignment_scores:
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                                                                 Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                 source
                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                 Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
1. .134365
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Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-7UN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases I to 134565)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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3 (bases 1 to 134365)
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                                                                                       Ratio:
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a 24497 c 25503 g 43951
                                                                                    26.00
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                                                                 Percent Identity: 100.000
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DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferretira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,G., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Sancos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Direct Submictory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boushyalter, B., Brown, A., Burkett, G., Castle, A., Choppel, Y. Colangelo M. Colling S. Collemore B. Corke B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, clone RP11-58M12
Unpublished
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                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 134743 bases at least Q30 Consensus quality: 139277 bases at least Q30 Consensus quality; 140814 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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                                                   51931
                                                                 47006 5183
51831 51930:
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40512 432
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62719: gap of 100 bp 75408: contig of 12689
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                                                                                                                                   43279: contig of 2768 bp in length 379: gap of 100 bp 46905: contig of 2768 bp in length
                                                                                                                                                                                      38820: contig of 38820 bp in length 920: gap of 100 bp 40411: contig of 1491 bp in length 511: gap of 100 bp 43279: contig of 2768 bp in length
                                         379: gap of 100 bp
46905: contig of 3526 bp in length
905: gap of 100 bp
51830: contig of 4825 bp in length
930: gap of 100 bp
62619: contig of 10689 bp in length
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  đđ
  in length
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US-08-973-363-8 x AC021449
                                                                                                                                                             ACCESSION
VERSION
                     REFERENCE
                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AC008531
                                                                                                                                                                                                                                                                                                                              seq_name:
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ORIGIN
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                                                                                                                  SOURCE
                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                      DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116197 CCGTGCAGACTACCTCATCAAATTACTT 116224
    AUTHORS
                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                           gb_htg:AC008531
                                                                                                                                                                                                                   Homo sapiens chromosome 5 clone 7 ordered rices
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                              Homo sapiens
                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                            7 ordered pieces.
                                                                                                                    numan.
                                                                                                                                                                  AC008531.3 GI:12830078
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92617 106409: contig of 13793 bp in length
106410 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length
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75509 9251
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51931. .62619
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40512, .43270
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clone_end:T7
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106510. .143079
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26246 c 26678 g
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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92516: contig of 17008 bp
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                                                                                                                                                                                                                                      CTC-480B11, WORKING
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DRAFT SEQUENCE,
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US-08-973-363-8 x AC008531
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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                                                                                                                                                            Align seg 1/1 to: AC008531 from: 1 to: 145659
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                                                    17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 139128 bases at least 040
Consensus quality: 14255 bases at least 020
Consensus quality: 142744 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148059; sum-of-contigs estimation
Quality coverage: 6.27 in 020 bases; pulse field gel estimation
Quality coverage: 6.4 in 020 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * the accession number will be preserved.

1 56174: contig of 56174 bp in length
56175 56274: gap of unknown length
1 56275 100874: contig of 44600 bp in length
100875 113127: contig of 12153 bp in length
113128 113227: gap of unknown length
113128 118190: contig of 6463 bp in length
113128 118190: contig of 463 bp in length
113129 118290: gap of unknown length
118291 119694: contig of 463 bp in length
118292 119694: contig of 1640 bp in length
118293 119794: gap of unknown length
119695 119794: gap of unknown length
119795 123297: contig of 3503 bp in length
1123298 123397: gap of unknown length
1123398 145659: contig of 22262 bp in length.
                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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1.000
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/clone_lib="CalTech human BAC library C"
26309 c. 27580 g 48609 t 600 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                 Length: 26
Gaps: 0
Percent Identity: 100.000
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Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; garose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* runs of M, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 5 clone RP11-36012, PROGRESS ***, 33 unordered pieces. AC091946
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1 (bases 1 to 19346)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5

Unpublished
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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                                                                               12461
12561
14612
14712
16382
                                                                                                                                                                                                                                                                                                                                                          1358: contig of 1358 bp in length
1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1957 bp in length
6020: gap of unknown length
7494: contig of 1474 bp in length
7494: contig of 1474 bp in length
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contig
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of 1487 bp in length
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alignment_scores:
Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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                                       CCGTGCAGACTACCTCATCAAATTACTT 87735
gb_pr:AC026778
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/db_xref="taxon:9606"
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LOCUS AC022121
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US-08-973-363-8 x AC026778/rev
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Quality:
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WI-13675 G23101
SHGC-58345 G38487
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joi Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, 2 (bases 1 to 195433)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
Direct Submission
                                HTG
                                                               AC022121
                                                                                 Homo sapiens chromosome 5
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Finishing Completed at Stanford Human Genome Center
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AC026778
AC026778.4 GI:14277282
Homo sapiens
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
/chromosome="5"
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US-08-973-363-8 x AC022121/rev
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89450 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 89401
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Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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4 (bases 1 to 219289)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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SHGC-103595 G57841
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
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Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute.
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/clone="CTD-2007H13"
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/db_xref="taxon:9606"
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-LOOPEXT-0.000 -GAPOP-4.500 -GAPEXT-0.050 -XGAPOP-60.000
-XGAPEXT-60.000 -FGAPOP-6.000 -FGAPEXT-7.000 -START-1
-MATRIX-0.000 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-0.190 -TANS-human40.cd1 -LIST-45 -DOCALIGN-200
-THR_SCORE-QUAlity -THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
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-DEV_TIMEOUT-120 -MARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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Database sequences: 1736436
Database length: 858457221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block: Query: US-08-973-363-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: Aug 3, 2002 7:18 AM
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                   Sequence 1316 BP; 492 A; 208 C;
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            17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
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Length: 41
Gaps: 0
Percent Identity: 100.000

306

G; 304 T; 6 other;

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The chicken CHD-W gene (AMT42754) acting alone or in conjunction with the closely related CHD-1A gene (AMT42771) is suggested to initiate femala development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997 (first entry)
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121.84
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144.
162.
165.
178.
189
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alignment_block:
US-08-973-363-8 x AAT42751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42751
                                                                                                                                                                                           Quality: 41.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1188
    4080
                                                                                                                                                                                                                                                                                                                                                                The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = AV1an) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffiths
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicken CHD-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42751;
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                                                                                                                                                                                                                                                                                                                                Sequence 6608 BP; 2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCACAGAGACTTGCTGGTGCA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex determination; chromodomain-Helicase-DNA binding 1 Avian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromodomain-helicase-DNA binding genes determine sex — used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds
                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tiwari B;
                                                                                       AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-GB01341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA; 6608 BP
                                                                                       from: 1
                                                                                                                                                                                           Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                1207 C;
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                                                                                                                                                                                                                                                                                                                              1459 G; 1653 T; 0
                                                                                                                                                                                           : 41
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                other;
  4129
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seq_documentation_block:
ID AAT42757 standard;
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                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     key Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chick CHD-1A gene fragment
                                                                                                                                               Claim
                                                                                                                                                                         birds
                                                                                                                                                                                                                                                      Griffiths R,
                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHD-1A; CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42757;
Sequence 153 BP;
                         embryo,
                                                                                                                                                                                                                  P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                     05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                         WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                             1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757
                                                                                                                                               8; Fig 3; 76pp; English.
                                                                                                                                                                      chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
                          foetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                          etc.
                                                                                                                                                                                                                                                                                                            95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W chromosome;
                                                                                                                                                                                                                                                                                                                                      96WO-GB01341
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and are ignored in the translated
acid sequence given in Fig 3"
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
Α;
                         and to manipulate the sex of progeny
40 C;
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G;
24 T; 0 other;
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amino
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alignment_block: US-08-973-363-8 x AAT42757

Percent Similarity:

Align seg 1/1

to:

AAT42757

from:

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to:

153

alignment_scores:

Quality:

Ratio:

34.00 1.000 100.000

Percent

Identity:

100.000

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alignment_scores:
Quality: 34.00
Ratio: 1.000
Percent Similarity: 100.000
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AAT42758 standard; DNA; 153
                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A - Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bird; sex determination; chromodomain-Helicase-DNA binding CHD-IA; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT42758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 la 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA 153
                                                                                                                                                                                                                                                                                                                                                                                                           chromodomain-helicase-DNA binding genes determine sex in used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95GB-0011439
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                                                                                                                                  56 A; 36 C; 31 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
     Percent
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Length: 34
Gaps: 0
Identity: 100.000
                                                                                                                               30 T; 0 other;
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seq_documentation_block:
ID AA742759 standard: DN
XX
AC AA742759;
XX
AC AA742759;
XY
AC AA742759;
XY
CHD-W; W CHD-W gene
XX
Bird; sex determinat:
XX
Bird; sex determinat:
XX
CHD-IA; CHD-W; W Chrx
XX
OS Parus major.
XX
FH Key
FT misc_difference 52..!
FT misc_difference 52..!
FT misc_difference 52..!
FT misc_difference 52..!
FT //*ta;
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FT misc_difference 52..!
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US-08-973-363-8 x AAT42758
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                                                         Bases 3855-3977 (AAR142756) of the mouse CHD-1 gene show homology to portlons of the chicken CHD-1A (A = Avian) gene (AAR142757), chicken CHD-W (W refers to the W chromosome) gene (AAR142758) and and the great tit CHD-W gene (AAR142759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAR142751) and CHD-W (see also AAR142754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1A; CHD-W; W chromosome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS INNOVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 la 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95GB-0011439
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          60 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 153
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"bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
             33
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             ç;
             29 T;
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             0 other;
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alignment_scores

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seq_documentation_block:
ID AAV59280 standard;
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                           The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangelctasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g.
                                                                                                                                                                                                                  Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomersees caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                             Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-1998
                                                                                                                                                                                     Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                WPI; 1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altered telomere repeat binding factor 1 gene
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                                                                                                                                                                                                                                                                                                                                                                           (UYRQ ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9836066-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                for expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 27.00
Ratio: 1.000
Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sLeuLeuAsnLysAspLeuAlaArgLysGlu 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
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                                                                                                                                                                                                                                                                                                                                             De Lange
                                                                                                                                                                                                                                                                                                                                                                             ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                                          98US-0018628
97US-0800264
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..1311
recombinant proteins or where testing, eliminating the need
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                                                                                                                                                                                                                                                                                                                                             Van
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Gaps: 0
Identity: 100.000
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                intended for subsequent
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alignment_scores:
Quality:
 ID AAT42756 standard;
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US-08-973-363-8 x AAV59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1287
                                                                                                                                   Avian
birds
       Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W wrefers the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bird; sex determination; chromodomain-Helicase-DNA binding
CHD-1; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1311 BP;
                                                                                                        Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                         Griffiths R,
                                                                                                                                                                                                                                 (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                 05-JUN-1996;
                                                                                                                                                                                                                                                                                                                               WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rArgAlaAspTyrLeuIleLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGTGCAGACTACCTCATCAAACTA 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                     1997-043127/04
DB; AAW08146.
                                                                                                                               chromodomain-helicase-DNA binding genes determine - used for sex determn. and to control sex of prog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                          Tiwari
                                                                                                                                                                                                                                                         95GB-0011439
                                                                                                                                                                                                                                                                                 96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 52..81
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                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 A;
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L.000
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manipulate
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                                                                                                                                   progeny
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progeny.

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seq_documentation_block:
ID ABL06443 standard;
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Ratio: 1.000
Percent Similarity: 100.000
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                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01076-ABL30511), expressed DNA sequences (ABL01040-ABL16175) and the encoded proteins (ABB07737-ABB72072).
           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                       Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
P-PSDB; ABB62340.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL06443 standard; cDNA; 6240 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 sLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                          Li PWD,
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                          Myers EW;
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alignment_scores:

Quality: Ratio:

11

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seq_documentation_block:
ID ABL06442 standard
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US-08-973-363-8 x ABL06443
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4205 AAGCCCCAGGCCAAGCAGCTGCAGACGCGTGCC 4237
                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 13808.
                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
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DB; ABB62339.
                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                          The invention
                                                  WIPO
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alignment_block:
US-08-973-363-8
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30-JUN-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

26-JUL-2000

14-AUG-2000

15-AUG-2000

23-AUG-2000

23-AUG-2000

23-AUG-2000

23-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000
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04-FEB-2000;
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19-MAY-2000;
07-JUN-2000;
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seq_documentation_block:
ID AA157603 standard; cDNA; 421 BP.
XX
AC AA157603;
XX
DT 19-OCT-2001 (first entry)
XX
DE Human colorectal cancer antiqen cD
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Quality: 10.00
Ratio: 1.000
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US-08-973-363-8 x AAK88882
                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI57603
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
  Human colorectal cancer antigen cDNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 421 BP; 148 A; 78 C; 127 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1198; 986pp; English.
                                                                                                                                                                                                                           146 AAGCAGCTACAGACCCGAGCGGATTACTTG 175
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US-08-973-363-8 x AAI57603
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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P-PSDB; AAM38625.
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                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase; cell signalling; inflammation; carcinoma; diabetes; human X-linked agammaglobulinaemia; nonspherocytic haemolytic anaemia; artherosclerosis; glioma; restenosis; cholera-based septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
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                                                    Au-Young J,
                                                                                                                                               07-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides polynucleotides which encode novel protein Kinase homologs expressed in various human cells and tissues. The present sequence represents the clone 23789 cDNA fragment derived from a human inflammed adenoid cDNA library. The cDNA encodes a protein kinase which shows homology to the CHKPRNK chiken tyr kinase. Cells and host cells can be used for recombinant production of the protein kinase homolog. The recombinant proteins may be used to raise antibodies for use as anti-kinase therapeutics. Oligonucleotides based on the polynucleotide sequences, i.e. probes and antisense constructs, the peptides and antibodies are claimed to be useful as tools for studying signalling cascades in cells and proteins, and for identifying inhibitors (drugs) to treat diseases and inflammatory conditions associated with abnormal kinase expression. Diseases that are claimed to be treatable include human x-linked agammaglobulinaemia, carcinomas, restrenceds. Cholora-hased seatic shock are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAV33521 from: 1
Penn SG,
                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #10208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA61903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AAACTGCTCAACAAAGACCTGGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 252 BP; 63 A; 70 C; 72 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes, gliomas, restenosis, cholera-based septic shock, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Columns 29-30; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human kinase poly:nucleotide(s) and recombinant products - useful for identification of modulators of the enzyme, and treatment of diseases associated with abnormal kinase expression
                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                 30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LysLeuLeuAsnLysAspLeuAla 31
Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                 ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                        2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.000
Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 100.000
Rank DR;
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Single exon nucleic acid probes for analyzing gene expression in

human

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alignment_scores:
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ID AAK10214 standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-973-363-8 x ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK10214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: ABA61903
                                                                                                                          04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-023659.

04-0CT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. For this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                            epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 10205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK10214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 544 BP; 144 A; 128 C; 88 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 10208; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52.
                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                              WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK10214 standard; DNA; 544 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.000
                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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                                                               Rank DR;
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brains

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seq_documentation_block:
ID AAK36112 standard; DNA; 544 BP.
XX
AC AAK36112;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed exon
KW Human; bone marrow expressed exon
KW Human 2001; 2001WO-US00668.
XX
DF 20-ANY-2001; 2001WO-US00668.
XX
DF 21-SEB-2000; 2000US-0180312.
PR 21-SEB-2000; 2000US-06184687.
PR 21-SEP-2000; 2000US-0632566.
PR 21-SEP-2000; 2000US-0636359.
PR 21-SEP-2000; 2000US-0236359.
PR 21-SEP-2000; 2000US-068408.
PR 30-JUN-2000; 2000US-080312.
PR 26-MAY-2000; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EX CCCCCCX PX PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-973-363-8 x AAK10214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK36112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure generation in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 544 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4;
   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone marrow expressed single exon probe SEQ ID NO: 10669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                       Example 4; SEQ ID NO: 10669; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful for zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone marrow expressed exon; gene expression analysis; probe; rray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO: 10205; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                  Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ი</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544
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SSSSS
                                                                                                alignment_block:
US-08-973-363-8 x AAK36112
                                                                                                                                                                                                 alignment_scores:
                                                                                                                                         Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                Align seg 1/1
                                                                                                                                                                                                                                                                           samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                Sequence 544 BP; 144 A; 128 C;
                    21 TyrLeuIleLysLeuLeuAsnLys
                                                                  to:
                                                                  AAK36112
                                                                   from: 1
                                                                                                                                            Length: 8
Gaps: 0
Percent Identity: 100.000
                                 28
                                                                                                                                                                                                                                                88 G;
                                                                   .
0
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gb_est2:BI035224
gb_est1:AW961278
gb_est2:BG757172
gb_est1:AW364689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est1:BB830733
gb_est1:BB834922
gb_est2:BE739967
gb_est1:AW997058
gb_gss:CNS04DVG
gb_gss:CNS04DVG
gb_est1:AF881342
gb_est1:CNS04DVG
gb_est1:CNS04DVG
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Query leng
Database:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database sequences: 13736207
Database length: -1841457050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block:
Query: US-08-973-363-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: Aug 3, 2002 5:46 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM of: US-08-973-363-8 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est1:AL659353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search time (sec): 4311.510000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-Frame-ppn. model -DEV=xlh -O202_080123_19814/app_query.fasta_1.638 -Q=/cgn2_1/USPf0_spool/US08973363/runat_01082002_080123_19814/app_query.fasta_1.638 -DB-EST -O2PMT-fasta_ SUPFIX-volip2n.rst -GAPOP=4.500 -GAPEXT-0.000 -GAPEXT-0.000 -GAPEXT-0.000 -GAPEXT-0.000 -GAPEXT-0.000 -GAPEXT-0.000 -GAPEXT-0.000 -YGAPOP=60.000 -YGAPOP=60.000 -GAPOP=60.000 -GAPOP=60.00
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3. 6e-19
5. 4e-19
5. 4e-19
5. 8e-19
9. 6e-19
9. 6e-19
1. 0e-14
1. 1e-14
2. 1e-14
2. 1e-14
2. 1e-14
3. 2e-10
0. 061
                                                                                                                                                                                                                                                                    0.1966
0.2081
0.2190
0.2257
0.2275
                                                                                                                       | ALL65935 ALC65935 XGC-neurula | ALC64594 ALC64594 XGC-egg Silu | ALC64594 XGC-egg Silu | ALC64594 XGC-egg Silu | ALC64594 XGC-egg Silu | ALC64595 BB450756 BB450756 BIKEN Full-le | BB46105 BB46105 BB46105 RIKEN Full-le | BB4973967 601905770F1 NIH, MGC_54 ALC64594 XGC-egg Silu | ALC64597                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Documentation
H53564 yq86h11.s1 Soares fetal
BI035224 QV2-NN2003-220401-631-
AW961278 EST373350 MAGE reseque
BG757172 602710541F1 NIH_MGC_48
AW364689 PM3-DT0037-231299-001-
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gb_est2:H38315
gb_est1:AM354153
gb_est1:AA427958
gb_est1:AA477850
gb_est1:AA477856
gb_est2:BF901677
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seq_documentation_block:
LOCUS AL644594
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LOCUS AL659353
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alignment_block:
US-08-973-363-8 x AL659353/rev
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Ratio: 1.000
Percent Similarity: 100.000
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Silurana tropicalis
Sularana tropicalis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinxton, Cambridgeshire, CB10 1SA, UK Email: tropésanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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Sanger Centre
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/Clone_lib="XGC-neurula"
/Clone_lib="XGC-neurula"
/dev_stage="neurula"
//ab_host="Escherichia coli DH10B"
//ab_host="Scherichia coli DH10B"
//ab_host="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

Bight results the stage of th
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Gaps: 0
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| H38315 yp70c06.r1 Soares adu
| AW354153 32640 MARC 2PIG Sus
| AA427958 zw50a01.r1 Soares_t
| BH228000 1006143E10.x1 1006
| AA477885 zu34e05.r1 Soares o
| BF901677 PM4-MT0201-091200-0
        EST 07-NOV-2001
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REFERENCE
AUTHORS
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US-08-973-363-8 x AL644594
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AL644594
AL644594.1
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DKF2p313J1040_r1 313 (synonym: hlcc2) Homo
DKF2p313J1040 5', mRNA sequence.
AL601246
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 430)
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Sanger Centre
Bloecker,H., Boecher,M.,,S.
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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                                                                                                                                                     Homo sapiens
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/clone=lib="XGC"
/clone_lib="XGC"
/clone_
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/db_xref="taxon:8364"
/clone="L1E1d12"
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                             and Wiemann
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alignment_block:
US-08-973-363-8 x AL601246
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ORGANISM
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LOCUS AI890775
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                wm95f11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDI_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1; mRNA sequence.
                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No sl sequence available.
This clone (DKFZp31331040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
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Contact: Bloecker
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                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                               Unpublished (1997)
                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="DKF2p313J1040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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/db_xref="taxon:9606"
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On Jun 29, 2000 this sequence version replaced gi:8811286. Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehtro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
Mus musculus
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Location/Qualifiers
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Insert Length: 1924 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2443725"
/clone_lib="NCI_CGAP_UTC?"
/clone_lib="NCI_CGAP_UTC?"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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alignment_block: US-08-973-363-8 x BB155356

Align seg 1/1 to: BB155356

from: 1 to: 619

alignment_scores: Quality:

Quality: 26.00 Ratio: 1.000 Percent Similarity: 100.000

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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.;

Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki,Y.

RIKRN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Shibata,K., Itoh,M., Carninci,P., Sugahara Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. II (2), 281-289 (2001) KONGO, S., Shinagawa, A., Satto, T., Kiyosawa, H., Yammanka, I., Aizawa K., Pikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues
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        194
                                                                contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGACTCTTTTTTTTTTTTTTTTTTV 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="thymus"
/dev_stage="16 days neonate"
/lab_host="DH10B"
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japrel: 81-45-503-9222
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Arakawa, T., Carninci, P., Fukuda, S.,
                                                              Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed.
                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiysawa, H., Yamanaka, I., Alzawa
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9216
Email: genome-res@g
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                                                        prepare mouse tissues
                                                                                                                                                                                                      further details.
                                                                                                                                                                                                                             Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                             Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with duman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                        Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                     library was prepared and sequenced in Mouse Genome
                          Location/Qualifiers
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ORGANISM
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US-08-973-363-8
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LOCUS AU125712
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481 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
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                1532-3 Yana, Kisarazu,
Tel: 81-438-52-3951
                                                                                                                                     HRI human cDNA project (Ota,T., Saito,K., Yamamoto,J., Nakamura,Y., Sugano,S., Isogai,T.)
                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                           Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU125712 NT2RM4 Homo sapiens cDNA clone
Fax: 81-438-52-3952
                                                                          Genomics Laboratory
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                                                       Helix Research Institute
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                                                                                                 Takao Isogai
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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Nakamura,Y., Nishikawa
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                                    292-0812, Japan
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Nishikawa, T., Nagai
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Ratio: 1.000
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1 (bases 1 to 1028)

NHH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601436060F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921087 5',
                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/note-"vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagali, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Ratio:
                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-att2-Qv3-BN0047-230
200-102-d03xt3-2000-02-3&r4-1)
Seq primer: puc 18 forward.

is primer: puc 18 forward.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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AW996787.1 GI:8257021
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High quality sequence stop: 337.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Average insert size 2 kb. Library con
Technologies."
a 205 c 238 g 198 t
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (O.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0047"
/dev_stage="Adult"
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Ratio:
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
Hayatsu, N., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.,
2001)
                                                                                                                                                                    Email: genome res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-9216
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BB834922
BB834922.1
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                                                                                                                                                                                                                                                                                              Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Ishii, Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozanae, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                  1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                       Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                     Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                2001)
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  URL:http://genome
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genome-res@gsc.riken.go.jp,
tp://genome.gsc.riken.go.jp/
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: 1.000
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96 c 108 g 96 t
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Percent Identity: 100.000
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                                                                                                           Yokohama, Kanagawa 230-0045, Japan
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seq_documentation_block:
LOCUS BF239967
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US-08-973-363-8 x BB834922
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                     homan.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 821)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishkawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (200)

Konno,H., Fukunishiy, Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                     BF239967.1 GI:11153890
                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              601905170F1 NIH_MGC_54
CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/cell_line="RCB-0527 Jyg-Mc(B)"
a 99 c 108 g 100 t
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                           821 bp r
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                              nRNA linear EST 14-NOV-2000 cDNA clone IMAGE:4133129 5',
                                                 MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                   TITLE
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                                                                                                 JOURNAL
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BASE COUNT ORIGIN

FEATURES

source

REFERENCE AUTHORS TITLE

COMMENT

ACCESSION VERSION SOURCE ORGANISM

DEFINITION

17

KEYWORDS

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alignment_block:
US-08-973-363-8 x BF239967
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Quality: 21.00
Ratio: 1.000
Percent Similarity: 100.000
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LOCUS AW997058
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||||||||||||
| 53 CATCAAATTACTT 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCCGATAAAAAACCACAAGCAAAACAGTTGCAGACCCGTGCAGACTACCT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW997058.1
EST.
                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         686 bp mRV
QV3-BN0047-150400-152-c03 BN0047 Homo
AW997058
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov k
plate: LLCM1033 row: k column: 18
High quality sequence stop: 562.
Location/Qualifiers
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
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// bouble-stranded cDNA was prepared from cell line RNA.
// adaptors were used in cloning as follows: 5'
// adaptor sequence: 5'-ACTCTAGACGCCATATGGCC-3' and 3' adaptor
// sequence: 5'-ATTCTAGACGCCAGCCGCCATATGGCC-3' and 3' adaptor
// sequence: 5'-ATTCTAGACGCCAGCCGCCATG-GT(30)BN-3'
// (where B = A, C, Or G and N = A, C, G, Or T). Average
// insert size l.5 kb (range 0.9-4.0 kb). 15/15 colonies
// contained inserts by PCR. This library was enriched for
// full-length clones and was constructed by Clontech
// Laboratories (Palo Alto, CA)."
                                                                                                                     Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:8257292
                                                                                                                 Acad. Sci. U.S.A. 97
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                     (7), 3491-3496 (2000)
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omo sapiens cDNA,
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ACCESSION
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LOCUS CNSO4DVG
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ORIGIN
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                                           REFERENCE
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                                                                                                      TITLE
                                                                                                                                                                                                                                                                                     ORGANISM
                                                              JOURNAL
                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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Ratio:
                                                                                                                                                                                                 Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                             AL286261
AL286261.1 GI:8024707
                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis genome survey sequence T7 end of clone 103K08 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150400-152-c03st3=2000-04-15&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                    Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot, Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                               Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                      Roest-Crollius, H.,
                                                                                                                                                                                 (bases 1 to 856)
                                         (bases 1 to 856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
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lius,H., Jaillon,O., Das:
Fizames,C., Wincker,P.,
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                  Dasilva,C.,
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ilva,C., Bouneau,L., Fisher,C.
Brottier,P., Quetier,F.,
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SOURCE

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TITLE
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http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Email: asimpson@ludwig.org.br
This sequence was derived from the
                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                   Contact: Simpson A.J.G.
                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                   Fax: +55-11-2707001
                                                  Tel: +55-11-2704922
                                                                                     Rua Prof. Antonio Prudente 109,
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Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=pMO&t2=pMO-ETO208-031200-001-fi2at5=2000-12-03&t4-1)

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High quality sequence stop: 128.
Location/Qualifiers
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High quality sequence stop: 128.
Location/Qualifiers
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gb_pat: A58685
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Database sequences: 1797656
Database length: 187333701
Search time (sec): 4908.870000
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-Q=/Cgn2_1/USPf0_spool/USO8973363/runat_01082002_080123_19828/app_query.fasta_1.638
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316 | A58896 Sequence 15 from Patent 6608 | A58891 Sequence 10 from Patent 6872 | AFROVASY Gallus gallus Chromo-153 | A58684 Sequence 3 from Patent No. 153 | A58685 Sequence 4 from Patent No. 153 | A58685 Sequence 4 from Patent No. 153 | A58685 Sequence 4 from Patent No. 153 | A58685 Sequence 3 from Patent No. 154 | AFROVASY 2 Homo sapiens Chromo-15456 | AC01262 Homo sapiens Chromo-15456 | AC01262 Homo sapiens Chromo-1556 | AC01262 Homo sapiens Chromo-1556 | AC02121 Homo sapiens Chromo-1558 | AC02178 Homo sapiens Chromo-1559 | A58683 Sequence 3 from Patent No. 1559 | A58683 Sequence 3 from Patent No. 1559 | AFROVATOR CHROMO-1559 | AC01865 Drosophila melanogaster 16430 | AC01985 Drosophila melanogaster 16400  | AC01985 Drosophila m
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153 | A58686 Seque
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6608 | A58691 Seque
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                          Sequence 15 from Patent A58696
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Griffiths, R. and Ti
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1. .153
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/db_xref="taxon:32644"
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Patent: WO 9639505-A 15 12-DEC-1996; ISIS INNOVATION (GB)
                                                               1 (bases 1 to 1316)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 9639505-A 5 12-DEC-1996; ISIS INNOVATION (GB) Other publication AU 5906996 961224
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AR055725 Sequence 2 from pa
AR058275 Sequence 2 from pa
1 AR058275 Sequence 2 from pa
1 U33284 Human protein tyrosi
AF053890 Rattus norvegicus
1 S80542 related adhesion foc
D45854 Rattus norvegicus mR
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US-08-973-363-9 x A58696
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ORIGIN
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LOCUS A58691
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US-08-973-363-9 x A58691
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Location/Qualifiers
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Griffiths, R. and Tiwari, B.
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/db_xref="taxon:32644"
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LOCUS AF004397
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TITLE
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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
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Griffiths,R. and Kor
Direct Submission
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                 KTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPOMNAVVYLGDITSRN
HIRTHEMMHPQTYRLKENILLTTYEILLKDKS FIGGLYGVEAHRLKNIDSSLLY
RTLIDFKSNHRLLITTGPFLONSLKELMSLHFINPEKFSSWFIGVDEAHRLKNIDSSLLY
RTLIDFKSNHRLLITTGPFLONSLKELMSLHFINPEKFSSWFIGVDEAHRLKNIDSSLLY
LHKELEPFLLRRVKNDVEKSLPAKVEQILRMEMSALOKOYYKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCHHCYLIKPDDWEFYNNCEALGHLIRSGKLIILDKLLILRLR
ERGNRVLIFSOMVYMLDILABYLKYROFPFORLDGSINGELKROALDHFNAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLOAQARAHRIGOKKQVNIYRLYTKGS
WEEDILERAKKKNYLDHLYIGRADTTGKTVLHTGSTPSSSTPFNKEELSAILKGALBE
LFKEPBGEBGEPGEMDIDEILKRAFTENENEPGPLTVGDELLSOFKVAHFSNMDEDDIE
LEPBRINSRNWEEIIPESORRRIEEEEERQKELEEIYMLPRMRNCAKQISFNGSBGRRSR
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DSESAEDGDKSSCEESEDYEPKNKYKSHKPPSRIKPKSGKKSTGOKKRQLDSSEEEE
DDDEDYDKRGSRQATVWYSYKAEEETKTDSDDLLEVCGEDVPQTEEDEFETIEKTHD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHHNTWETEET
LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
                                                                             SRRYSGSDSDSTTERKRPKKRGRPRTTPRENIKGFSDAETRRFTKSYKKFGGPLERLD
AVARDAELVDKSETDLRRLGELVHNGCTKALKDNSSGQERAGGRLGKVKGPTFRISGV
QVNAKLVISHBEELAPLHKSTPSDPEERKRYVTPCHTKAAHFDIDWGKEDDSNLLVGI
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CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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SQSGSSDSESGSGSGSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
HĽHXXIXTEKENEEK PEPDIGIXKEAEEK RETKEKENKRELKREKKEKEDKKELKEKD
                          RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSVK
                                                        YEYGYGSWEMIKMDPDLSLTQKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQ
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/note="CHD protein with hydrophilic domain
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/function="role in
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228. .5654
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/db_xref="GI:2501846"
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/db_xref="taxon:9031"
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on the Z chromosome
(CHD-Z) mRNA, compl
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us-08-973-363-9 x A58684
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Quality:
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US-08-973-363-9 x AF004397
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LOCUS A58684
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                Align seg 1/1 to: A58684 from: 1 to: 153
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Patent: WO 9639505-A 3 12-DEC-1996; ISIS INNOVATION (GB) Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3 from Patent WO9639505
A58684
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2446 a
                                                                                                                                                                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
58 a 40 c 31 g 24
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/gene="CHD-Z"
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1 1223 c 1520 g 1683 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
THVIRNPVERLKETTNHDDSSROSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKREY
SAFSNGKDHRDWDHYKQDSRYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
SDHRIHSDHSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
HRSPFEHSSDHKSTPEHTWSSRKT"
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Gaps: 0
Percent Identity: 100.000
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100.000
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COMMENT

TITLE

FEATURES

KEYWORDS

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JOURNAL
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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    Quality:
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LOCUS A58685
DEFINITION Sequence 4 fi
ACCESSION A58685
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US-08-973-363-9 x A58685
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 sLeuLeuAsnLysAspLeuAlaArgLysGlu 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 5349)

Delmas, V., Stokes, D.G. and Perry, R.P.

A mammalian DNA-binding protein that contains a chromodomain and a SNF2/SWIZ-like halicase domain

Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                                                                                                                                                                                                                                                                              Mouse DNA-binding protein
L10410 X66028
L10410.1 GI:455014
DNA binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other publication AU 5906996 961224.
Direct Submission Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 9639505-A 4 12-DEC-1996;
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Griffiths, R. and Ti
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/db_xref="taxon:32644"
36 c 31 g 30
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1. .153
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Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                 5349 bp mRNA linear in (CHD-1) mRNA, complete cds
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alignment_block:
US-08-973-363-9 x MUSCHD1X
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KEYWORDS
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ORIGIN
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                                                                                                                                                                                             seq_name:
                                                          ACCESSION
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                                                                                                                                                                                                                                                        CCGTGCAGACTACCTCATCAAACTACTT 4103
                                                                                                                                                                                          gb_pr:AF006513
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Ratio:
                                                    Homo sapiens CHD1 mRNA, AF006513
                             AF006513.1 GI:2645428
                                                                                                              AF006513
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CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKG
SVEEDILERAKKKMVLDHLVIQRNDTTGKTVLHTGSAPSSSTPFNKEELSAILKFGAE
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YKTLIDFKSNHRLLTGTPLQNSIKELMSLLHFIMPEKRSSWEDEHHGKGREYGYA
SLHKELEPFLLARVKKDVEKSLPAKVEĞILKEBMSALQKQYYKWILTRYKALSKSK
GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSSGKLILLDKLLIRL
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IAHSNOKSAAGLEDYYCKWQGLEYSECSWEDGALISKKRQTCIDEYFSRNQSKTTDFK
DCKVLKQPFREYALKKOPSYIGGHEGLELDYDLNGLINBLAHSWCKGSCILADEWG
GKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDINSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT"
1 1067 c 1319 g 1224 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLSEREQLEHTRQCL1KIGDH1TECLKEYSNPEQIKQWRKNLWIFVSKFTEEDARKLHKLYKHAIKKRQESQQNSDQNSNVATTHVIRNPDMERLKENTNHDDSSRDSYSSDRHLS
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QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSRRYSGSDSDSISEKKPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERL
DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSGTERAGGRLGKVKGPTFRISG
VQVNAKLVIAHEDELIPLHKSIPSDPERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG
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ELEPERNSKNWEEIIPEEQRRRLEEEEERQKELEEIYMLPRMENCAKQISFNGSEGRRS
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1.000
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DDEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEDEEFETIERVM
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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171. .5306
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/db_xref="taxon:10090"
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Gaps: 0
Percent Identity: 100.000
                                                                              complete cds.
                                                                                                         5947 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 5349
                                                                                                         mRNA
                                                                                                           linear
                                                                                                           PRI 27-NOV-1997
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alignment_block: US-08-973-363-9 x AF006513

Percent Similarity:

Align seg 1/1 to: AF006513

from: 1

to: 5947

alignment_scores:

Quality:

Ratio:

26.00 1.000 100.000

Gaps: Percent Identity:

Length:

26 0 100.000

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AUTHORS
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AUTHORS
BASE COUNT
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Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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RLREGRUYLIFSOMVRHLDILÆYLKYROF PPORLDGSIKGELRKQALDHFNAEGSE
DFCFLLSTRAGGLGINLASADTYV IFDSDWNPONDLOAQARAHRIGOKKOVNIYRLVT
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AEELFKEPEGBEDGEPQEMDIDEIIKKAETHENEPGPLYVGDELLSQFKVANFSNMDED
DIELFEDRNKKWWEEIIPEDORRRLEEBEERQKELEEIYMLPKWENCAKOISFNGSEGR
RSRSRRYSGSDSDSISEGKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKDCKVLKQRPRFVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEM
GLGKTIQTISELNYLFHBHQLYGPFLLVVPLSTLTSWQRBIQTWASQMNAVVYLGDIN
SRNMIRTHEWTHHQTKRLKFNILLTTYBILKDKAFLGGLUWAFIGVDEAHRLKNDS
LLYKTLLDFKSUHRLLTTGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYG
VASLHKELLEPFLLRVKKDVEKGLPAKVUQILBMEMSALQKQVXITTRNYKALSKG
VASLHKELLEPFLLRVKKDVEKGLPAKVUQILBMEMSALQKQVXITTRNYKALSKG
                                                                                                                                                                                                                                                                                                        RLDAIARDAELVDKSETDLRRLGELVHNGCIKALKDSSSGTERTGGRLGKVKGPTFRI
SGVQVNAKLVISHEEELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLL
IGIYEYGYGSWEMIKWDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKK
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                                                                                                                                                                                                        GLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
                                                                                                                                                                                                                                        EALSGAGSSKRRKARAKKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
ERSKKSSVSDAPVHITASGEPVPISEESEELDQKTFSICKERMRPVKAALKQLDRPEK
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KKQQQQQQQQQHQASSNSGSEEDSSSSEDSDDSSSEVKRKKHKDEDWQMSGSGSPSQS
                                                                   RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT
                                                                                                                                                                    KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSDSESEEEREKSSCDETESDYEPKNKVKSRKPQNRSKSKNGKKILGQKKRQIDSSEE
                                                                                                    RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
                                                                                                                                       YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAB87381.1"
/db_xref="GI:2645429"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="5q15-21; near WI-5811"
1. .5947
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/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MNGHSDEESVRNSSGESSQSDDDSGSASGSGSGSSSGSSSDGSS/
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PRI 21-JUL-2001

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seq_name: gb_pr:AC012624
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US-08-973-363-9 x AC092372/rev
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LOCUS AC092372
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                                                     26882 CCGTGCAGACTACCTCATCAAATTACTT 26855
                                                                                                                                              26932 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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Ratio:
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Estimated Total Number of Errors is 0.
MOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
Location/Qualifiers
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Mainut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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1 (bases 1 to 101220)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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DOE Joint Genome Institute.
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/db_xref="taxon:9806"
/db_cref="toxon:9806"
/chromosome="5"
/clone="RPII-8MM12"
/ 18862 c 17827 g 30409 t
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Percent Identity: 100.000
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US-08-973-363-9 x AC012624
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    Quality:
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                                                                                                                                                                                                                                                                                                             seq_name: gb_htg:AC021449
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LOCUS AC012624
     REFERENCE
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Ratio: 1.000
Percent Similarity: 100.000
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On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
1. .134365
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143079)
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Submitted (01-70N-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                     Homo sapiens
                                                                                                                                                                                                              AC021449 143079 bp DNA linear HTG 10-SEP-2000 Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTD-2082117, complete sequence.
AC012624
                                                                                                               AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT
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DOE Joint Genome Institute.
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a 24497 c 25503 g 43951
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JOURNAL REFERENCE AUTHORS

TITLE

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REFERENCE AUTHORS TITLE

KEYWORDS

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COMMENT

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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Tonsensus quality: 140814 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project Information Center project name: L5154 Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                              38821 38920: gap of 100 bp 38921 40411; contig of 1491 bp in length 40412 40511; gap of 100 bp 40512 43279; contig of 2768 bp in length 4280 43379; gap of 100 bp 43280 43695; contig of 3526 bp in length 45906 47005; gap of 100 bp 100 bp 51830; contig of 3526 bp in length 47006 51830; contig of 4825 bp in length
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                                92616:
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                                                                                                                    75508:
                                                                                                            930: gap of 100 bp in 62619: contig of 10689 bp in 719: gap of 100 bp in 75408: contig of 12689 bp in 508: gap of 100 bp
                                                                    08: gap of 100 bp
92516: contig of 17008 bp in
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alignment_block:
US-08-973-363-9 x AC021449
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LOCUS AC008531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                         116197 CCGTGCAGACTACCTCATCAAATTACTT 116224
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                                                                                                                                                                                                                                                                                         gb_htg:AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                              1 (bases 1 to 145659)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
2 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                           AC008531.3 GI:12830078
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                              AC00853
                                                                                                                                                                                                                          AC008531 145659 bp
Homo sapiens chromosome 5 clone
                              Unpublished
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Homo sapiens
                                                                                                                                                 numan
                                                                                                                                                                                                             7 ordered pieces.
                                                                                                                                                                                                                                            AC008531
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106510 143079: contig of 36570 bp in length.
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75509 92516
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51931. 62619
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CTC-480B11,
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DRAFT SEQUENCE,
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alignment_block:
US-08-973-363-9 x AC008531
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seq_name: gb_htg:AC091946
                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                        Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                         Align seg 1/1 to: AC008531 from: 1 to: 145659
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                            46820 CCGTGCAGACTACCTCATCAAATTACTT 46847
                                                                                    46770 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 46819
                                                                                                                                                                                                                                                                                                                                                                                                  source
                                           17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                 Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
Center Project Name: 369535
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Center: Joint Genome Institute
Center Code: JGI
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145659: contig of 22262 bp in length.
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LOCUS AC091946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 18475 bases at least Q20
Consensus quality: 18475 bases at least Q20
Consensus quality: 18475 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* is soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ------Genome Center Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo-
l (bases 1 to 19346)
DEE Joint Genome Institute.
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DOE Joint Genome Institute.
Direct Submission
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2668
2768
3824
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5921
6020: gap of unknown length
7494: contig of 1474 bp in length
7594: gap of unknown length
9096: contig of 1502 bp in length
9196: gap of unknown length
10260: contig of 1064 bp in length
10360: gap of unknown length
12560: gap of unknown length
14611: contig of 2100 bp in length
14711: gap of unknown length
14711: gap of unknown length
16381: contig of 1670 bp in length
16981: gap of unknown length
16981: gap of unknown length
16981: gap of unknown length
18068: gap of unknown length
20434: contig of 2366 bp in length
20534: gap of unknown length
20534: gap of unknown length
20534: gap of unknown length
23515: contig of 2366 bp in length
23515: contig of 3948 bp in length
23515: contig of 3948 bp in length
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1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1997 bp in length
6020: gap of unknown length
6020: gap of unknown length
7494: contig of 1474 bp in length
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                                                 seq_name: gb_pr:AC026778
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Ratio: 1.000
Percent Similarity: 100.000
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Homo sapiens chromosome 5 clone CTC-428I11, ACO26778
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/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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/db_xref="taxon:9606"
/chromosome="5"
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117571: contig of 6605 bp in length
117671: gap of unknown length
123738: contig of 6007 bp in length
12338: gap of unknown length
130583: contig of 6745 bp in length
130583: contig of 6745 bp in length
130683: gap of unknown length
141544: contig of 10861 bp in length
141544: gap of unknown length
169109: contig of 77465 bp in length
169109: gap of unknown length
169209: gap of unknown length
193446: contig of 24237 bp in length
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Gaps: 0
Percent Identity: 100.000
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LOCUS AC022121
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                   REFERENCE
                                                                                                                                                                                                                                        seq_name: gb_pr:AC022121
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Ratio: 1.000
Percent Similarity: 100.000
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WI-13675 G23101
SHGC-58345 G38487
SHGC-103595 G57841.
                                                                                                                                             219258 bp
Homo sapiens chromosome 5 clone
AC022121
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence by DOE Joint Genome Institute
www.jgi.doe.gov
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Submitted (24-MAR-2000) Production Sequencing Facility,
Submitted (24-MAR-2000) Production Sequencing Facility,
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                       Homo sapiens
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AL Submitted (219258)

2 (bases 1 to 219258)

22 (bases 1 to 219258)

AL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission

AL Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

22 4 (bases 1 to 219258)

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission

AL Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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STS Content: WI-5811 G04974 WI-5813 G239487 G38487 G38487 SHGC-103595 G57841.
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                 Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                             Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1a (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW0146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
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to: 153

Length: 34
Gaps: 0
Percent Identity: 100.000

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alignment_scores:
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ID AAT42754 standard; cDNA; 1316 BP
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                                                                     alignment_block:
US-08-973-363-9 x AAT42754
                                                                                                         Quality: 34.00
Ratio: 1.000
Percent Similarity: 100.000
                                           Align seg 1/1 to: AAT42754
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                                                                                                                                                                                                                                    The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken CHD-W gene
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                                                                                                                                                                                                Sequence 1316 BP; 492 A;
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1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                       chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
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; chromodomain-Helicase-DNA binding on the W chromosome;
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alignment_block:
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ID AAT42751 standard;
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                                                                                                                                                                                                                                                                                                                                      The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
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CDS
                                                                                                                                                                                                                                                                                      Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromodomain-helicase-DNA binding genes determine sex — used for sex determn, and to control sex of progeny
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; chromodomain-Helicase-DNA binding on the W chromosome; ss.
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Align seg 1/1

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AAT42751

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seq_documentation_block:
ID AAT42757 standard; DNA; 153 BP.
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Quality: 27.00
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                                                                                                                                                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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P-PSDB; AAW08147.
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CHD-IA; CHD-W; W chromosome; ss.
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                                                                                                                                                                     Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
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Percent Identity: 100.000
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US-08-973-363-9 x AAT42757
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ID AAT42758 standard; DNA; 153 BP.
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                           Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42751) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                  WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                 Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers misc_difference 52.81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42758;
Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                     P-PSDB; AAW08148
                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy 24
                                                                                                                                                                                                                                                                                                                                                              95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
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alignment_scores:

Quality: 27.00 Ratio: 1.000 Percent Similarity: 100.000

Length: 27
Gaps: 0
Percent Identity: 100.000

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seq_documentation_block:
ID AAV59280 standard;
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US-08-973-363-9 x AAT42758
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                                    The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeichasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequent
                                                                                                                                                                                                            Claim 14; Page 110-111; 163pp;
                                                                                                                                                                                                                                                                                                                                                                 Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                             also
                                                                                                                                                                                                                                                                        Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, us
                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW59280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       telomere; ageing; ataxia telangeictasia; Down's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altered telomere repeat binding factor 1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 sLeuLeuAsnLysAspLeuAlaArgLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                                            inhibit shortening of telomerases caused by ageing so used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:AAV59280
                                                                                                                                                                                                                                                                                                                                                                  De Lange T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                            tor
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97US-0800264
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/product= "A-TRF"
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1..1311
                          testing, eliminating
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                                                                                                                                                                                                                                                                                                                                                                  Steensel B;
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                                                                                                                                                                                                             English
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                         the need
                          for transformation.
                                                                                                                                                                                                                                                          or disease,
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Sequence 1311 BP;

441 A; 257 C; 316 G;

297 T; 0 other;

Sequence 153

BP;

61

P.

37

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27

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28 T;

0 other

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seq_name:
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US-08-973-363-9
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1237 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                               Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify
                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42756 standard;
                                     the sex of
                                                                                                                                                                                                                   P-PSDB; AAW08146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHD-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 rArgAlaAspTyrLeuIleLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGTGCAGACTACCTCATCAAACTA 1311
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                                                                                                                                                                                                                               1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex
                                                                                                                                                     8; Fig 3; 76pp; English.
                                                                                                                                                                             chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHD-W;
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                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determination;
                                     an embryo, foetus etc. and to manipulate the sex of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 153 BP
                                                                                                                                                                                                                                                                                                                                                                                                          "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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Percent Identity:
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US-08-973-363-9 x AAT42756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL06443
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLISTOS-ABLISTS). expressed DNA sequences (ABLO1840-ABLISTS) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
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                                                                 (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL06443 standard; cDNA; 6240 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other.
                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABB62340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
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alignment_scores:

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alignment_block:
US-08-973-363-9 x ABL06443
alignment_block:
US-08-973-363-9 x ABL06442
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ID ABL06442 standard; cDNA; 9933 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL18140-ABL16175) and the encoded proteins (ABB70773). (ABB70773).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO the sequence of the sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
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disease; chronic colitis;
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XX
AC AA157603;
XY
DT 19-OCT-2001 (first entry)
XX
DE Human colorectal cancer antigen
XX
Human; colorectal cancer; color
XX
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynuclectides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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P-PSDB; AAM93109.
                                           Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
                                                                                      Human colorectal cancer antigen cDNA SEQ ID NO: 67.
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US-08-973-363-9 x AAI57603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SXXCCCCCCCCCXXXPTTXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
Human kinase poly:nucleotide(s) and recombinant products - useful for identification of modulators of the enzyme, and treatment of diseases associated with abnormal kinase expression
                                                                                                                                                                                                                                                                                human X-linked agammaglobulinaemia; nonspherocytic hartherosclerosis; glioma; restenosis; cholera-based CHKFRNK chiken tyr kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of colorectal cancer antigens. These are shown in AAI57647-AAI57619 and AAM38669-AAM386641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or recture present sequence is a colorectal cancer antigen coding sequence of the present sequence is a colorectal cancer antigen coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide disorders related to and also for testing
                                                         WPI; 1998-556387/47.
                                                                                                                                            07-AUG-1996;
                                                                                                                                                                     07-AUG-1996;
                                                                                                                                                                                                                             US5817479-A
                                                                                                                                                                                                                                                                                                                                                       Clone 23789 cDNA fragment encoding a human protein kinase homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AAGCAGCTACAGACCCGAGCGGATTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 421 BP; 148 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-457727/49.
P-PSDB; AAM38625.
                                                                                                               (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                   06-OCT-1998
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                            Protein kinase; cell signalling; inflammation; carcinoma; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LysGlnLeuGlnThrArgAlaAspTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV33521
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                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                     Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI57603
                                                                                                                                            96US-0700575
                                                                                                                                                                       96US-0700575
                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA;
                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; 522pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
the
and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon and detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                     Hawkins PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 127 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing and/or prognosing rectum including colorectal cale.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 T; 7 other;
                                                                                     Wilde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                     cc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .00
                                                                                                                                                                                                                                                                                                                 haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and/or rectum
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alignment_block:
US-08-973-363-9 x AAV33521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID ABA61903 standard;
  seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides polynucleotides which encode novel protein kinase homologs expressed in various human cells and tissues. The present sequence represents the clone 23789 cDNA fragment derived for from a human inflammed adenoid cDNA library. The cDNA encodes a protein kinase which shows homology to the CHKFRNK chiken tyr kinase. Vectors and host cells can be used for recombinant production of the protein kinase homolog. The recombinant production of the polynucleotide sequences, i.e. probes and antisents based con the polynucleotide sequences, i.e. probes and antisense constructs, the peptides and antibodies are claimed to be useful as tools for the polynucleotide sequences, i.e. probes and antisense constructs, the peptides and antibodies are claimed to be useful as tools for studying signalling cascades in cells and proteins, and for identifying inhibitors (drugs) to treat diseases and inflammatory conditions associated with abnormal kinase expression. Diseases that are claimed to be treatable include human x-linked agammaglobulinaemia, or the polynucleotide agammaglobulinaemia, atthemations, earchinomas, diabetes, gliomas, restenosis, cholera-based septic shock, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAV33521 from: 1
                                                                                                                                                                                      04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-MUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234567.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
Human genome-derived single exon nucleic acid probes useful for
                                                WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #10208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA61903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA61903 standard; DNA; 544 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 AAACTGCTCAACAAAGACCTGGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 252 BP; 63 A; 70 C; 72 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Columns 29-30; 30pp; English.
                                                                                             Penn SG,
                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LysLeuLeuAsnLysAspLeuAla 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                             Hanzel DK,
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                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 8
Gaps: 0
Percent Identity: 100.000
                                                                                             Rank DR;
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seq_documentation_block:
ID AAK10214 standard; DNA; 544 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: ABA61903 from: 1
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                                                                                                                                                                                           04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0508408; 30-JUN-2000; 2000US-0508408; 03-AUG-2000; 2000US-0532366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0234559; 04-OCT-2000; 2000GB-0024263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing gene expression in human fetal liver -
                                                  Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe SEQ ID NO: 10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK10214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 544 BP; 144 A; 128 C; 88 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 10208; 639pp + sequence listing; English.
           Example 4; SEQ ID NO: 10205; 650pp + Sequence Listing; English
                                                                                             WPI; 2001-483446/52.
                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epilepsy; cancer;
                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.000
                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 8
Gaps: 0
Percent Identity: 100.000
                                                                                                                             Rank DR;
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seq_documentation_block:
ID AAK36112 standard; Dh
XX
AC AAK36112;
XX
DT 06-NOV-2001 (first (
XX
Human bone marrow ext
XX
Human; bone marrow ext
XX
OS Homo sapiens.
XX
O9-AUG-2001; 2001WO-U
XX
O9-AUG-2001; 2000US-U
PR 20-AUG-2000; 2000US-U
PR 20-AUG-2000; 2000US-U
PR 21-SEP-2000; 2000US
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US-08-973-363-9 x AAK10214
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon;
microarray; cancer; leukaemia; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                          Example 4; SEQ ID NO: 10669; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrLeuIleLysLeuLeuAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCTGATAAAGTTATTAAATAAG
                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful for
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234683.
2000US-0234683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 544 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
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9b_est1:BB461065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database sequences: 13736207
Database length: -1841457050
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Query: US-08-973-363-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
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-OB-EST -OPNT-fastap -SUFFIX-olip2n.rst -GAPOP-4.500
-GAPEXT-0.050 -MINMATCH-0.100 -LOOPEL-0.000 -LOOPEXT-0.000
-GAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-60.000 -XGAPEXT-60.000
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
-ELOP-6.000 -DELEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
-ELOP-6.000 -DELEXT-7.000 -XFART-1 -MATRIX-0ligo
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-quality
-THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext
-HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-SC8973333_GCGN1_1.2938 -NCEU-6 -ICPU-3 -LONGLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ALGS953 ALGS953 XGC-neurula | ALGS953 ALGS953 ALGS953 XGC-neurula | ALGS953 ALGS953 XGC-neurula | ALGS953 ALGS953 ALGS951 ALGS953 ALGS951 ALGS951 ALGS954 ALGS956 ALGS954 ALGS956 ALGS954 ALGS956 ALGS954 ALGS956 ALGS954 ALGS956 AL
1 N49703 Y V3403.31 Soares fetal AA305759 EST176834 Colon carcin AA305759 EST176834 Colon carcin AL870450 w146605.x1 NCI_CGAP_UT H661027 YF50f12.51 Soares fetal A1915135 w150e08.x1 NCI_CGAP_CC EM365726 ES320017000E12 Subtract EM365102 ES320023000E9 Subtract EM366134 ES32003000H9 Subtract EM366634 ES32003000H9 Subtract EM366634 ES320023000H9 Subtract EM366634 ES320023000H9 Subtract EM366624 ES320023000H9 Subtract EM366624 ES320023000H9 Subtract EM366629 ES320023000H9 Subtract EM366429 ES320023000H8 Subtract EM366429 ES320031-230401-631 AW961278 EST373350 MAGE reseque EG757172 602710541F1 NHH MGC_449 AW364689 PM3-DT0037-231299-001-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Documentation
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9b_9ss:AQ794671
9b_est1:AA177423
9b_est2:H38315
9b_est1:AA477858
9b_est1:AA477856
9b_est2:BF901677
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AUTHORS
TITLE
JOURNAL
COMMENT
             seq_documentation_block:
LOCUS AL644594
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US-08-973-363-9 x AL659353/rev
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                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AL659353 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Battachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing primer: SP6
This sequence is from a xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL659353 XGC-neurula Silurana
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//bb_xref="taxon:8364"
//bb_xref="Taxon:8364"
//clone=_Tib="XGC-neurula"
//dev_stage="neurula"
//dev_stage="neurula"
//abb_bost="Escherichia coli DH10B"
//note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
//note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI and the 5', end and NotI at the 3', end."

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                 mRNA
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linear

EST 07-NOV-2001

DEFINITION

AL644594 XGC-egg

Silurana tropicalis cDNA clone L1E1d12 5', mRNA

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ACCESSION
VERSION
KEYWORDS
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US-08-973-363-9 x AL644594
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ORIGIN
                       REFERENCE
                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                           seq_name: gb_est1:AL601246
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                                                                                  SOURCE
ORGANISM
                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                               DEFINITION
                                                                                                                            KEYWORDS
                                                                                                                                                  VERSION
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.

1 (bases 1 to 645)
1 (bases 1 to 645)
                                                                                                                                                                   DKFZp313J1040_r1 313 (synonym: hlcc2) Homo DKFZp313J1040_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 430)
                                                                                                                            EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing primer: PlC This sequencing trimer: PlC This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               western clawed frog.
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AL644594.1
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                                                                                Homo sapiens
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  Bloecker,H.,
                                                                                                        human.
                                                                                                                                               AL601246.1 GI:15164752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="xGC-egg"
/dev_stage="egg"
/lab_host="Escherichia coli XLI-blue"
/lab_host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cD/note="Vector: pCS107; Site_1: EcoRI; A+ RNA from egg.
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
a 125 c 156 g 141 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="L1E1d12"
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Boecher, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
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Brandt, P.,
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Mewes, W.,
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                                         Hominidae;
                                                                                                                                                                                                          sapiens cDNA clone
Weil,B.
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                                                             Euteleostomi;
                                                                                                                                                                                                                                EST 14-AUG-2001
and Wiemann
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ACCESSION
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AUTHORS
TITLE
                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est1:AI890775
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US-08-973-363-9 x AL601246
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                                                                                                                      JOURNAL
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AI890775

wm95f11.x1 NCI_CGAP_Ut2 Homo sap similar to SW:CHD1_HUMAN 014646

PROTEIN 1 ;, mRNA sequence.
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                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                          AI890775
AI890775.1 GI:5595939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone (DKFZp313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIPS
                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                            EST
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This is the 5' sequence of the clone insert
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                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                           Tumor Gene Index
cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: Greg Lennon, Ph.D.
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cDNA-collection"
a 81 c 86 g 100 t
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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1.000
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Percent Identity:
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                                                              Ph.D.,
                                                                                                                                                                                                                                             Euteleostomi;
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6, 1405
                                                              Michael
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LOCUS BB155356
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                         JOURNAL
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Hiramoto, K., Horl, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nemura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takai, T., Sogabe, Y., Suzuki, H., Tagami M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

AL Unpublished (2001)

AL Unpublished (2001)

On Jun 29, 2000 this sequence version replaced gi:8811286.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB15356 RIKEN full-length enriched, 16 days menat EST 18 BB15356 RIKEN full-length enriched, 16 days meonate thymu musculus cDNA clone Al30024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 619)

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Insert Length: 1924 Std Error: 0.00
Seq primer: -40Up from Gibco
Bigh quality sequence stop: 418.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
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/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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Align seg 1/1 to: BB155356

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alignment_block:
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Tgawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Hayashizakiy.

RIKNN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno. H., Fukunishiy.

Y. and Hayashizakiy.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo. S., Shinagawa, A., Salto. T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Laxawa, Laxawa, Laxawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Laxawa, Lax
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Further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/dev_stage="16 days neonate"
/dev_stage="16 days neonate"
/lab_host="pil0B"
/nore="Site_1: Sal1; Site_2: BamHI; cDNA library was
/nore="Site_1: Sal1; Site_2: BamHI; cDNA library was
/noreared and sequenced in Mouse Genome Encyclopedia
/project of Genome Exploration Research Group in Riken
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/rikethold for the project of the pilot 
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/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp,

Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                          encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
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                                                          prepare mouse tissues
                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU125712 MT2RM4 Homo sapiens cDNA clone NT2RM4002061
                 1532-3 Yana, Kisarazu,
Tel: 81-438-52-3951
                                                                                                 Unpublished (2000)
Contact: Takao Iso
                                                                                                                                        Saito, K., Yamamoto, J., Naki, Y., Sugano, S., Isogai, T.)
                                                                                                                                                                                   Isogai, T.
HRI human cDNA project (Ota, T.,
                                                                                                                                                                                                                          Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuh
                                                                                                                                                                                                                                                                                                                                                                                                AU125712.1 GI:10950428
Fax: 81-438-52-3952
                                                        Helix Research Institute
                                                                               Genomics Laboratory
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1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rike
                                                                                                   Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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spinal ganglion"
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="D130070B13"
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Gaps:
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                                      292-0812, Japan
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l 5', mRNA
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US-08-973-363-9 x AU125712
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Ratio: 1.000
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                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1028)

NHH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Eukaryota; M
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/cell_tine="NY2"
/cell_line="NY2"
/note="Vector: pME185FL3; mRNA from uninduced NT2 neuronal precursor cells"
a 149 c 196 g 207 t 2 others
/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
/tlssue_type="melanotic melanoma"
/tlssue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-08-973-363-9 x BE895133
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1 (bases 1 to 337)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bah,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             хмээо/в/
QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA,
AW996787
                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl7tl=6t2=QV3-BN0047-230 200-102-d03&t3-2000-02-23&t4-1)
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                                                                                                                                                                                                                                                                                                               Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brazil
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Average insert size 2 kb. Library co
Technologies."
a 205 c 238 g 198 t
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
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                                                                                                                                                                                                                                    Location/Qualifiers
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Gaps: 0
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Library constructed by Life
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                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Satio,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Yoshihide Hayashizaki
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216
Email: genome-res@g
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Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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m Jyg}-MC(B) cDNA Mus musculus cDNA clone G930033J21 3', mRNA
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                                                                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 821)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone_lib="RIKEN [full-length enriched, mammary gland
/close_1527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
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/db_xref="taxon:10090"
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KEYWORDS

FEATURES

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BASE COUNT
ORIGIN
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LOCUS AW997058
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagqi,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagqi,M.A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Ratio:
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1033 row: k column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed sequence tags % \left\{ 1\right\} =\left\{ 
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Clone distribution: MGC clone distribution information can be
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//db_xref="rtxon:9606"
//clone="IMAGE:4133129"
//clone="Ib="NIH_MGC_54"
//tissue_type="from chronic myelogenous leukemia"
//tissue_type="from chronic myelogenous leukemia"
//tissue_type="from chronic myelogenous leukemia"
//lab_host="DH10B (Tl phage=resistant)"
//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Clont
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JOURNAL REFERENCE
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AUTHORS
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                                                                                                                             TITLE
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AL286261
                                                                                                                                                                                                                                                                                                                                   GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
Seq_primer: puc 18 forward
  Roest-Crollius, H., Jail
Bernot, A., Fizames, C.,
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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High quality sequence stop: 678.
Location/Qualifiers
                                                                         Unpublished
                                                                                               Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                     Weissenbach,J.
                                                                                                                                                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fis
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
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Tel: +55-11-2704922
                                                                                                                                                                                                                                           Tetraodontidae;
                                                                                                                                                                                                                     (bases 1 to 856)
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1 (bases 1 to 129)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
Email: asimpson@ludwig.org.br This sequence was derived from the
                                                                                                                                                                                                                                                                          Simpson, A.J
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Unpublished
                                           Fax: +55-11-2707001
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2520	CTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCCA	2461	γQ
2460	GATTTTAACAAGGAATTATAAAAGCCCTCAGTAAAGGTTCAAAAAGGCAGTACCTCAGGCT	2401	рb
2460	ATTTTAACAAGGAATTATAAAGCCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGC	2401	Qy
2400	CTAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATTACAAGT	2341	В
2400	naggttgaacaaattctgaggatggaaatgagtgcattgcagaagcaatattacaag		Q
2340	AAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTAGAAAAGTCTTTACCTG	2281	망
2340	AGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTAGAAAAGTCTTTACC	2281	Qy
2280	GGGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGAGTATGGTTATGCAAGTCTTCACA	2221	뭥
2280	GGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGAGTATGGTTATGCAAGTCTTCAC	2221	Qy
2220	ATTOCCTCAAAGACTIGTGGTTGTTGGTTGATTCATCATGCAGAAAAATTTTCCTCCT [2161	B 6
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2160	GACTITAATAGACTITAAGTCCAACCATGGACTTCTGATTACTGGAACCCCACTGCAAA 	2101	D Q
7	つかつ ボール・プロ・プロ・プロ・プロ・プロ・プロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ・グロ	_	?

5400	CAGATCACAAAAGTACACCTGAACATACATGGAGTAGCCGGAAGACATAACAAAGACTGA	5341	В
5400	AGATCACAAAAGTACACCTGAACATACATGGAGTAGCCGGAAGACATAACAAAGACTG		γQ
5340	AGAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGAACACTCAT	5281	рь
5340	STCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGAACACTC	5281	Qy
28		2	DЬ
5280	CTCAGACTGGCAAATGGACCACAGAGCTTCTGGTAGTGGCCCGAGGTCACCACTAGAT	5221	VΩ
22		σ	g d
5220	CAGATCACCGTTCCACTTCAGAATACAGCCATCATAAATCTTCGAGAGATTATAGATAC	5161	Qy
5160	ACTTAAAAGACAGCCGGGGTCATTCAGATCACCGCTCCCATTCAGACCACAGGATACACT	5101	망
5160	AAAAGACAGCCGGGGTCATTCAGATCACCGCTCCCATTCAGACCACAGGATACAC		Qγ
5100	GTAAACATAGAAAGTTAGATGACCACAGGAGCAGAGACCACAGGTCAAACCTGGAAGGAA	5041	Db
5100	ATAGAAAGTTAGATGACCACAGGAGCAGAGACCACAGGTCAAACCTGGA	5041	Qy
5040	ATGGAAAAGATCACAGAGACTGGGATCACTACAAACAGGACAGCAGATACTACAGTGATA	4981	ф
5040	TGGAAAAGATCACAGAGACTGGGATCACTACAAACAGGACAGCAGATACTACAGTGAT		δō
98		N	gb .
4980	TCAGGGAGATGCTTACAAGAAAAGTGACTCCAGGAAAAGGCCATATTCAGCCTTCAGT	4921	Q Q
	GGGACAGTTATTCTTCTGATAGACATTTATCACAATACCATGATCATCACCAAGACAGGC	4861	밁
4920	GGACAGTTATTCTTCTGATAGACATTTATCACAATACCATGATCATCACAAAGACAGG	4861	Qγ
4860	TAATCAGAAATCCAGATGTGGAAAGACTGAAGGAGACTACAAACCATGATGATAGTAGCA	4801	밁
	AATCAGAAATCCAGATGTGGAAAGACTGAAGGAGACTACAAACCATGATGATAGTAGC	4801	δõ
4800	AGCGCCAAGAGTCTCAGCAACACAATGACCAAAACATTAGCAGCAATGTGAATACACATG	4741	망
4800	CGCCAAGAGTCTCAGCAACACAATGACCAAAACATTAGCAGCAATGTGAATACACAT	4741	δ
4740	CCAAGTTTACAGAATTTGATGCCAGAAAGCTGCACAAACTCTACAAACATGCAATCAAAA	œ o	B 8
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4680			B 2
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4620	AGCTGGAACATACTAGGCAGTGTCTAATCAAAATTGGGGATCACATTACAGAATGCCTGA 	4561	B 5
56	TGTCAAAGCAGCACTGAAACAGCTGGATAGACCAGAGAAGGGCCTTTCTGAAAGGGAG	jö) b
6	CTGTCAAAGCAGCACTGAAACAGCTGGATAGACCAGAGAGAG	Ü	γ
4500	AGAAGAATCTGAAGAACTCCATCAGAAGACATTTAGTGTGTGCAAAGAAAG	4441	Db
4500	CAGAAGAATCTGAAGAACTCCATCAGAAGACATTTAGTGTGTGT	4	Оу
4440	AAATTCCATTGCTGGATACTCCAGTTCATATTACTGCAACCAGTGAACCAGTTCCTATCT	4381	Db
4440	AATTCCATTGCTGGATACTCCAGTTCATATTACTGCAACCAGTGAACCAGTTCCTATC	4381	Qy
4380	ATGAGGAGGAGGATAACAAGGTAAATGAAATGAAATCTGAAAATAAAGAAAATCTAAAA		В
4380	AGGAGGAGGATAACAAGGTAAATGAAATGAAATCTGAAAATAAAGAAAAATCT	4321	δ.
4320	TAAAAGAAGAATAAAGAGTGATTCTTCACCACAACCCTCAGAAAAATCTGATGAAGATG	4261	В

6480 6480	GCCAAGATTCATTGTAAATCCATTTGTTTTCCCTCTTTAACATGGGCAATAATGTCAAAT	6421 6421	Оу
6420	AGGTGCATTGGTTTAAAAGAAGGAAGTGTTCTATAGGTGAACACTTCAAAACCCAGATCA	6361	Qy
6420		6361	Db
6360 6360	TGATTGTTATATGAACAGTGAGAATATCCCACTCTAAACTGTGCCCTGGAAAGCTTTTC	ù ù	Qy Db
6300	TACATACCTGTTTTTGGTTGTTTATTTTATTTTTTTTTT	6241 6241	Qy
6240 6240	GTAAAAATGGGGAAGGGAATATTTTATTCCATTTAGTGCTCCTTTTTTATTGGATACTTT		Qу Db
6180	TCTTTTCACAAAGTCAGTATACCTTACATGTTTTAATAAATA	6121 6121	Qy Db
6120 6120	AAATGAGCTTTTTTCCGTCAGGCTTTTTTTGGCTGTTCCTTTCCCCAACAACTCAGGCCT	6061	Qy Db
6060	CAATTAAAAAAAAAAACACAACAAAACCAACAAATGGCTGTAAATTATTGTAAATTAATT	0 0	Qy Db
6000	TTTCTCCTGTTTGTGATCAGTTATAATGCCTTTTTATGAAACAAAC	5941 5941	Qy Db
5940	$\triangleright - \triangleright$	5881	Db
5940		5881	VQ
5880	AAGGACTTTGTTCACTTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCC	ω ω	Qy Db
5820	CTTATGTTTCAGGAAAGAATGGGGGATTTATTTTGTTTATTTCTTGGTAGAGAACTCTC	5761	Qy
5820		5761	Db
5760	TTTTGTAAATGAACACTTAAACACTGACCTGTG		Qy
5760			Db
5700-	GACCTCAACACTGCCCCTTTCAGACTGGATCTTACTATAAAACTCTTCATGTCAAAGTGG	5641	Qy
5700		5641	Db
5640	TGTGCTGCAAATGTTGTGGCACTTTTTTTTAAGAAATGGAAGATGTTTACTTTTACAGG	5581	Qy
5640			Db
5580	TGCAAGGTCTATTATCCCAACAGAAGAAAATATTTTTGTATTTAAAGTTTATGCTGCAC	5521	Qy
5580		5521	Db
5520	GACTIGAAAGATATGGACTGGATATTCTATCAGTAGCAGTATTGTTACTTCCTTTCCAGGA	5461	Qy
5520		5461	Db
5460	CATTITCTGGACCTICTTTITAGCCATATACAGTAAACTAACACAGTAATTGCCTTACAT	5401	Qy
5460		5401	Db

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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
97473516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Direct Submission Valence Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
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CKVLKORPRFVALKKOPSYIGGHESLELRDYOLNGLNWLAHSWCKGNSCILADEMGLG
KTIOTISFLNYLFHEHOLYGPFLLRVPLSTLTSWOREIOTWAPOMNAVVYLGDITSRN
                                                                FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKGS
VEEDILERAKKKWVLDHLVIQRWDTTGKTVLHTGSTPSSSTPFNKEELSAILKFGAEE
LFKEPEGEEQEPQENDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNWDEDDIE
                                                                                                                                                          MIRTHERMHPOTKRIKFNILLITYYEILLKOKSFIGGLNAAFIGVDSAHRIKNDSSLLY
RTLIDFKSNHRILITGTPLONSIKELMSLLHFIMPEKFSSWEDFEEEHGKGREYGYAS
LHKELEPFLLRRYKKDVEKSLPAKVEOILRHEMSALGKOYYKWILTENYKALSKGSKG
STSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQEALOHLIRSSGKIILLDKLLIRLR
                                                                                                                                                                                                                                                                                                                                                    DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
                                                                                                                                                                                                                                                                                                                                                                                                     LKKQQQQQKAASSDSGSEEDSSSSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGS
DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC60282.1"
/db_xref="G1:2501846"
/db_xref="G1:2501846"
/translation="MNGHSDEESVRNSSGESSRSDDDSGSASGSGSSSSSSSSSSSSSS
SQSGSSDSESGSSGSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="CHD-Z"
228. .5654
                         SRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERLD
                                                                                                                                        ERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDFC
                                                                                                                                                                                                                                                                                                                               LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="chromo-helicase-DNA-binding on the Z chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGY
                                              <u>LEPERNSRNWEEIIPESQRRRIEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRSR</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CHD-Z"
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                                                                                                                                        AAGACTGGCAAATGTCAGGGTCAGGGTCAGTATCAGGAACTGGTTCTGATTCTGAATCGG
                                                                                                                                                                                                                                                                                                                              AGCAACAGCAACAGCAAAAAGCAGCATCATCAGACAGTGGTTCAGAAGAGGACTCATCCA 600
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CGGAAGATGGGGATAAAAGCAGTTGTGAAGAAAGTGAATCTGACTATGAGCCAAAAAACA
                                                                                            AAGACTGGCAAATGTCAGGGTCAGGGTCAGTATCAGGAACTGGTTCTGATTCTGAATCGG
                                                                                                                                                                                      GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAGCATAAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGTCAAACGCATTACTTCGAAAACATACGGAGTACCAGAAAGGGGGATTCTTGACCTAC 180
                                                                                                                                                                                                                                  GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAAGCATAAAGATG
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HLHKKIKTEKENEEKPEPDIGIKKEAEEKRETKEKENKRELKREKKEKEDKKELKEKD
NKEKRENLYKESTQKEKEVKEEKNEMKSENLEKSKKIPLLDTPVHTATSEPVPISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CHD-2"
/note="short insert found in longer variant mRNA of CHD-2"
1 1223 c 1520 g 1683 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRSPFEHSSDHKSTPEHTWSSRKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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Pred. No. 0;
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1860 1860	1801 AACTGTATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTGACATCTTGGCAAAGAG	Оy
1800	1741 TGGGTCTGGGTAAAACAATACAAACAATTTCTTTTCTGAACTACCTGTTTCATGAACATC	Ф
1740 1740	1681 GATTGAATTGGCTCGCTCATTCATGCTGCAAAGGAAATAGTTGTATTCTTGCAGATGAAA 	Фр
1680 1680	1621 AGCAACCATCTTACATTGGAGGACATGAAAGTCTGGAGTTAAGAGATTATCAGTTAAATG	DP QA
1620 1620	1561 CTACTCCCTTTAAGGACTGCAAGGTTCTAAAACAGAGACCAAGATTTGTTGCACTGAAGA	Db Qy
1560 1560	ப் ப	Db Qy
1500 1500	1441 ACTACTATTGCAAATGGCAGGGTCTGCCTTACTCAGAATGTAGCTGGGAAGATGGTGGTCTC	Db 04
1440 1440	1381 ATCAAATAGTGGAAAGAATAATTGCTCATTCAAATCAAA	Qу
1380 1380	1321 CAGAAGATGTGGAATATTATAACTGCCAGCAGGAGCTTACAGATGATCTGCACAAACAA	Qу
1320 1320	1261 AACTGGACAACTACAAGAAAAAGGATCAGGAGACAAAACGCTGGCTG	ОУ
1260 1260	1201 TCCATAACACTTGGGAAACTGAAGAAACGCTGAAGCAACAAAATGTTAAAGGAATGAACA	Дy
1200 1200	1141 AAAAGTCAAAGGAGCTGGGAGAAATACAGTATCTTATTAAATGGAAAGGCTGGTCACACA	D Q
1140 1140	1081 CTGGTGCCTCAACCACCATCTATGCCGTTGAGGCAGATGGTGACCCAAATGCTGGGTTTG	ОУ
1080	1021 AAGATGAATTTGAAACTATAGAGAAGTTTATGGACAGTCGAATTGGCCGAAAAGGAGCCA	Оy
1020 1020	961 CCAAGACAGATTCTGATGATTTGCTGGAAGTTTTGTGGAGAGGATGTCCCACAGACTGAAG 	Оу
960	901 ATAAGAGAGGATCTCGTCGCCAGGCAACAGTGAATGTTAGTTA	ОУ
900	841 GACAGAAGAAGAGGCAACTTGATTCATCAGAGGAGGAGGAGGAGGATGATGAAGATTATG	ОУ
840 840	781 AAGTCAAAAGCCGTAAACCTCCAAGCAGAATTAAGCCAAAAAGTGGGAAAAAGAGCACAG 	Оу

3000	${\tt ATATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGA}$	2941	Qy
2940	CACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAAAAAACAGGTTA	2881	рb
2940	ACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAGAACAGGTT	2881	Qy
2880	TTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTGGAAC	2821	Db
2880	ATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTC	2821	Оу
2820	ATCATIT CAPTO CASANSSA CASASSATIT CISTITITIAN TO CISCA CASASSACTISSA ATCATIT CAPTO CASASSACA CASASSATIT CISTITITIAN TO CISCA CASASSACTISSA ATCATIT CAPTO CASASSACTIS CASASSACTICA CASASSACTIS CASASSACTICA CASASSACTIS CASASSACTIS CASASSACTICA CASASSACTICA CASAS	2761	dd Vy
5 6		,	> !
2760 2760	AGTTTCCCTTCCAGAGACTTGATGGATCAATAAAAGGGGAATTGAGGAAGCAAGC	2701 2701	Db
7	GATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCG	2641	Дb
2700	TGATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGCC	2641	Qy
2640	GGAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTTC	2581	Дb
2640	GAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTT	2581	Оу
58		52	Db
2580	AGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTAGCAGC	2521	Qy
2520	TTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCCAC TTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCCAC	2461	Db QY
4 6	GATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT	. 4	рь
	GGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT	4	Qy
2400	H-	2341	Db
2400	TAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATTACAAG	2341	Qy
2340	AGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTAGAAAAGTCTTTACCTG	2281	Dъ
2340	AGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTAGAAAAGTCTTTACCTG	2281	Qy
2280	GGGAAGATTTTGAAGAGGAGCATGGCAAAGGAGAGAGTATGGTTATGCAAGTCTTCACA	N	DЪ
2280	GGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGAGTATGGTTATGCAAGTCTT	2221	Qy
2220	ATTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCATGCCAGAAAAATTTTCCTCCT	2161	DЬ
2220	TCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCATGCCAGAAAATTTTTC	2161	Qy
16		10	Db :
2160	GACTTTAATAGACTTTAAGTCCAACCATCGACTTCTGATTACTGGAACCCCACTGCAAA	2101	0γ
2100	GGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAATGATGACTCTCTCT	2041	Db
2100	GGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAATGATGACTCTCTTCTGTAC	2041	Qy
2040	TACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGGTCTCAATT	1981	DЪ
2040	ACTICTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGGTCTC	1981	Qy
1980	GAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAACGATTAAAGTTTAACA	1921	Db
1980	AAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAACGATTAAAGTTTAAC	1921	Qy
Ñ		1861	Db
1920	GATTCAAACTTGGGCTCCTCAGATGAATGCTGTAGTTTACTTAGGAGATATAACTAG	1861	Qγ

2941 ARTITUTICGCTAGTCACAAAGGATCAGTGAAGAAGAATTCTGAAGAACCAGAAGAAACCAAGGATGAAGAACTTTTAGTAATTCAGAAGAACGACCAAGAAGAATTCTCAGAAAACTGTTCCAAGAACGACCAAGAAGAACTGTTCCAAGAACGACCAAGAAAACTGTTCCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAGAAAACTGTTCAAGAATTGAAAAACTGTTCAGAAAACTGTTCAAGAATTGAAAAAACTGTTCAAGAATTGAAAAAAAA
TRATCGCTAGTCACAAAGGATCAGTAGAAGAAGATATTCTTGGAGAAGAAGATTATCTTGGAAAGAAGATTATCTTGAAAAGCTCAGGAAAAACTGTTCAGAGAAGAAGATATTCTTGAGAAAACTGTTCAAAAGCTCTTGAAAAAACTGTTCAAAAGCTCTTGAAAAAACTGTTCAAAAGCTCTAGAAAAAACTGTTCAAAAGCTCTAGAAAAAAACTGTTCAAAAAAACTGTTCAAAAAAAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITION delta-crystallin enhancer binding protein, complete sequence.

10N 101316

N D14316.1 GI:391639

DS ORF2.

Gallus gallus (library: lambda gtll) 13 day embryo lens cDNA to mRNA, clone JFll.

IISM Gallus gallus (Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.

1 (bases 1 to 2292)

Thirary Complete Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Funahashi,J., Sekido,R., Murai,K., Kamachi,Y. and Kondoh,H. Delta-crystallin enhancer binding protein delta EFI is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (7e1:022-272-9499, Fax:022-272-3982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1994)
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            GOGOL_STATE-1

/GOGOL_STATE-1

                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="lens"
/clone_lib="lambda gt11"
/dev_stage="13 day embryo"
257, 1939
                                                                                                                                                                                                                                                                                                                                                                                       /note="beta-gal fusion protein binds to blocks HN fragment of delta-crystallin enhancer."
GRRSRSRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGP
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                  AGGAAATGGATATAGATGAAATCTTGAAGAGAGCTGAAACTCGGGAAAATGAGCCAGGTC
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RISGVOVNAKLVISHEEELAPLHKSIESDPEERKRYVIPCHTKAAHFDLDWGKEDDSN
LLVGIYEXAYGSWQCKVNGSRSQLUREILPDDPDRTPRQNSYRPVQTTSLNY"
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AF006659
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Griffiths,R., Double,M.C., Orr
A DNA test to sex most birds
Mol. Ecol. 7 (8), 1071-1075 (1
9837745
2 (bases 1 to 345)
Griffiths,R., Double,M., Kate,
Direct Submission
Submitted (02-JUN-1997) Zoolog
Glasgow G12 800, UK
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Gallus gall
Eukaryota;
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Gallus gallus C
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AF006659.1 GI:
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                    Location/Qualifiers
1. .345
/organism="Gallus gallus"
/db_xref="taxon:9031"
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(CHD-Z) gene,
                                                    zoology,
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1 111
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1 (bases 1 to 111)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Sequence 32 from Patent W09639505.
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/Codon_Start=1
/Codon_Start=1
/product="CHD-2"
/protein_1d="AAC69441.1"
/db_xref="Gr:3811117"
/translation="LPRMRNCAKQISFNGSEGRRSRSRRYSGSDSDSITERKRPKKRG
RPRTIPRENIKGFSDA"
a 60 c 76 g 109 t
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/db_xref="taxon:32644"
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/gene="CHD-Z"
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join(<1. .30,
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Nymphicus hollandicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Eukaryota; Metazoa; Neognathae; Psittaciformes; Cacatuidae;
Archosauria; Aves; Neognathae; Psittaciformes; Cacatuidae;
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binding protein 1 (CHD12) mRNA, partial cds.
AF181828.1 GI:5917752
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1 (bases 1 to 2754)

Fridolfsson,A.K. and Ellegren,H.
Molecular evolution of the avian CHD1
  A58684
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//Godon_start=1
//product="chromodomain helicase DNA binding protein 1"
//product="chromodomain helicase DNA binding protein 1"
//protein_id="And6025.1"
//bc.xref="ci:5917757"
//bc.xref="ci:5917757757"
//bc.xref="ci:5917757757"
//bc.xref="ci:59177577577577577
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<1. .>2754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Nymphicus hollandicus"
/strain="Lutino cockatiel"
/db_xref="taxon:13180"
/chromosome="2"
<1...>2754
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A58684
                                                                                                                                                                                                                        Submitted (30-AUG-1999) Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Norbyvagen
                                                                                                                                                                                                                                                          Fridolfsson, A.-K. and Ellegren, H. Direct Submission
                                                                                                                                                                                                                                                                                                                                               Fridolfsson, A.K. and Ellegren, H. Molecular evolution of the avian CHD1
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; C
Archosauria; Aves; Neognathae;
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Griffiths,R. and Tiwari,B.
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Conservative 0;
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              /product="chromodomain helicase
/protein_id="AAD56021.1"
/db_xref="GI:5917753"
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<1. .>2754
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                                                                                                     /gene=
                                                                                                                                                   /db_xref="taxon:103375"
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/db_xref="taxon:32644"
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                                                                                                                                                                 organism="Aegolius funereus"
translation="ELTDDLLKQYQIVERIIAHSNQKSAAGYPDYYCKWQGLPYSECs/
                                                                                       ne="CHD1W"
.>2754
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Neognathae; Strigiformes; Strigidae; Aegolius.
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Pred. No. 3.3e-40;
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1 (bases 1 to 5947)
Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                                                                Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Genome Research Institute, National Institutes of Health, 49 Convent Drive, Bethesda, MD 20892-4442, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens CHD1 mRNA, AF006513
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LRDYQLNGLNWLAHSWCKGNSCILADENGLGK'IQTISFLNYLHEHOLYGPFLLYVIL
LKDKYGLNGLNWLAHSWCKGNSCILADENGLGK'IQTISFLNYLHEHOLYGPFLLYVIL
LKDKSFLGGLNWVFIGVDEAHRLKNDDSLLYKTLIDFKSNHRLLITGTFIL
LKDKSFLGGLNWVFIGVDEAHRLKNDDSLLYKTLIDFKSNHRLLITGTPLONSLKELW
SLLHETMFEKFSSWEDFEEHGAGREFGYASLHKELRPFLLRWYKNDVEKSLPAKVEO
ILRMENGALQKQYYKHILTRNYKALSKGSKGSTSGFLNHMELKKCOHCYLIKPPDD
NEFYNKOBALQHLIRSSGKLILLDKLLIRLERGNRVLIFSQAVRMLDILABADTVVIFDSDM
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RKRYVIPCHTKAAHFDIDWGKEDDSNLLIGIYEYGYGSWEMIKMDPDLSLTQKILPDD
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164. .5293
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[. .5947
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                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                      /organism="Homo
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5836 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTTCATCACAAG 5895
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       Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DDE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (1988) 1 to 101220)
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DOE Joint Genome Institute.
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Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
www-shgc.stanford.edu
                                                                                                                                                                                                                                          DOE Joint Genome Institute and Stanford Human Genome Center.
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sapiens chromosome 5 clone RP11-58M12, complete sequence
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DFCFLLSTRAGGLGINLASADTVVIFDSDWNQAUDLQAARHRIGGKKQVMIYRLVT
KGSVEDIJLERAKKRWLDHLVIGRMDTGSTVLHTGSAPSSSTPFNKEELSAILKFG
KGSVEDIJLERAKKRWLDHLVIGRMDTGSTVLHTGSAPSSSTPFNKEELSAILKFG
KASVEDIJLERAKKRWLDHLVIGRMDTGSTVLHGREPQPLTVGDELLSQFKVANESUMDED
DIELEPENSKNWEEIIPEDQRRLEEEEPKREKELSGFKVANESUMDED
DIELEPENSKNWEEIIPEDQDRRLEEEEPKREKELSGFKVANESUMDED
DIELEPERNSKNWEEIIPEDQDRRLEEEERKIKGFSDAEIRREIKSYKKFGGPLE
RSSSRRYSGSDSDSISEGKREKKGGRPKTPRENIKGFSDAEIRREIKSYKKFGGPLE
RLDAIABDAELVDKSSTDLRRLGELVHRGCIKALKOSSSGTERTFGGRLGKVKCGFTFRL
SGVQVNAKLVISHEEELIPLKSIFSDEDERKARQYTPCHTKAAHFDLDMGKEDDSNLL
IGIYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKK
EALSGAGSSKRKAARKKNAMKSIKVKEEIKSDSSPLPSEKSDEDDDDKLSESKSDGR
EBSKKSSYDJAVHITASGEPVFISESSEDLOKTFFSKDEDDDDKLSESKSDGRR
EBSKKSSYDJAVHITASGEPVFISESSEDLOKTFFSKDEDDDDKLSESKSTEDPARKL
GLIEREDLEHTROCLIKIGDHTTECLKEYTNEDGIKOWRKNUMTFVSKFTEFDARKLIK
GLIEREDLEHTROCLIKIGDHTTECLKEYTNEDGIKOWRKNUMTFVSKFTEFDARKLIK
GLIEREDLEHTROCLIKIGDHTTECLKEYTNEDGIKOWRKNUMTFVSKFTEFDARKLIK
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FKDCKVLKQPFRYDALKQPSY IGGHEGLELEDYQLNGLWALAHSWCKGNSCILADEM
GLAKTIOTISELNYLLEHBLOLYQPFLLVPISTLYSWOREIOTWASOMNAVYLGDIN
SRNMIRTHEWTHHQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDS
LLYKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPERSSWEDEEBEHGKGREYG
YASLHKELEPFLLRFVKDVEKSLFAVYGQILKWAJLOKOYYKWILTHNYKALSKG
YASLHKELEPFLLRFVKDVEKSLFAVYGQILKDGALQHLIRSSGKLILLDKLIL
SKGSTSGFLNIMMELKKCONHCYLIKPDNNEFFYKGGALQHLIRSSGKLILLDKLIL
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YHDHKKDRHOGDSYKKSDSRKRPYSSFSNKADHDDHYKODSRYYSDREKHRKLDDH
RSKOHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDGWOND
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FMDCRIGRKGATGATTIIXAVEADGDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWET
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Db 12061 TITCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 12002
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82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-7UL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
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NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
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Mammalla; Eutheria; Primatės; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
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24497 c 25503 g 43951 t
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/chromosome="5"
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                  1.2%; Score 82; DB 9; Length 134365; 100.0%; Pred. No. 7.7e-30; Indels 0; Indels 0;
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PRI 21-JUL-2001

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RESULT 10 AC092372/c LOCUS

AC092372

KEYWORDS VERSION DEFINITION

ORGANISM

Homo sapiens

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BASE COUNT ORIGIN

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Query Match Best Local Similarity

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     * NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is
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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
McPheeters, R., Meldrim, J., Monnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Kothman, D.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
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Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
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Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Starge-Thomann, N.,
Rov, A., Santos, R., Severy, P., Spencer, R., Spencer, R., Severy, P., Spencer, R., Severy, P., Spencer, R., Severy, P., Spencer, R., Spencer, R., Severy, P., Spencer, R.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Perceira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gadara, S., Cant, G., Gage,D., Galagan,J., Gadara, S., Gage,D., Galagan,J., Gadara, S., Gage,D., Galagan,J., Gadara, S., Gage,D., Galagan,J., Gadara, G., Gage,D., Galagan,J., Gage,D., Galagan,J., Gadara, G., Gage,D., Galagan,J., Gadara, G., Gage,D., Galagan,J., Gala
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Homo sapiens, clone RP11-58M12
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 10, 2000 this sequence version replaced gi:7407963 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmer, A. and Zody
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Treat size: 14000. agraefs at least Q20
                                                                                                                                                                                                                            Quality coverage: 4.6 in Q20 bases; Quality coverage: 4.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L5154
Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
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Primates;
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Query Match
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                                   CTTGAATATTTAAATTCTGTAC 5917
CTTGAATATTTAAATTCTGTAC 131100
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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20: gap of 100 bp
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Consensus quality: 142556 bases at least Q20
Consensus quality: 142744 bases at least Q20
Consensus quality: 142744 bases at least Q20
Estimated insert size: 148080; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                  * This sequence will be replaced

* this sequence will be preserved.

* the accession number will be preserved.

* the accession number will be preserved.

* the accession number will be preserved.

* 56174 contig of 56174 bp in length

* 56275 100874 cantig of 56174 bp in length

* 56275 100874 cap of unknown length

* 100875 100974 gap of unknown length

* 100875 113127 contig of 44600 bp in length

* 113128 113227 gap of unknown length

* 113128 113227 gap of unknown length

* 113128 113227 gap of unknown length

* 118291 118290; contig of 4963 bp in length

* 118291 118290; gap of unknown length

* 118291 119694 contig of 4964 bp in length

* 119695 113297; contig of 3503 bp in length

* 113298 113397; gap of unknown length

* 123298 123397; gap of unknown length

* 123298 123397; gap of unknown length

* 123298 123397; gap of unknown length
     ch 1.2%; So 1 Similarity 100.0%; F 82; Conservative 0;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14559)
DOE Joint Genome Institute.
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE.
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                                                                                                                                     /organism="Homo sapiens"
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/chromosome="5"
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/clone="CTC-480B10"
a 26309 c 27580 g 48609 t
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Score 82; DB 2; Le; Pred. No. 7.7e-30; 0; Mismatches 0;
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     0;
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     74518 CTTGAATATTTAAATTCTGTAC 74497
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                                                 5896 CTTGAATATTTAAATTCTGTAC 5917
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WI-13675 G23101
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AC022121.6 GI:15375145
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/db_xref="taxon:9606"
/chromosome="5"
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. Match 1.2%; Score 82; DB 9; Length 2192
Local Similarity 100.0%; Pred. No. 7.4e-30;
nes 82; Conservative 0; Mismatches 0; Indels
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (26-JAN-2000) Mitchell Drive, Walnut Creek, CA 94598, US
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1 (bases 1 to 219258)
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3 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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HOMO Sapiens chromosome 5 clone CTD-2007H13, complete sequence.
AC022121
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1 42062 c 40933 g 64309 t
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403
                                                                                     GCTCATTCATGGTGCAAAGGAAATAGTTGTATTCTTGCAGATGAAATGGGTCTGGGTAAA 402
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Psittaciformes; Cacatuidae;
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Fridolfsson, A.-K. and Ellegren, H.
Direct Submission
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KKDKSFLGGLNAVFIGVDEAHRLKNDDSLLYKFLIFKSNHRLLTTGTPLQNSIRELM
SLLHFIMPERFKSSWEDFEEBHGKGREBGYASLHKELEPFLLARVKKDVEKSLDAKVED
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PFPGRLDGSIKGELRKOALDHFNAGESEDFCFLSTTAGGLGINLASADTVUTFDSW
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KTVLHTGSTPSSSTPFNKEELSAILKFGAEELFKEEPGDKLRWEEDIIPVKGRRIEEEERGKELKKLASHDTR
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/db_xref="taxon:13180"
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<1. .>2754
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IKALNDNSFVQERAAGRLGKVKGPTFRISGVQVNAKLVISHEEELAPLHKSIPSDPEE
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WEDGALIAKKFQACIDEYFSRNLSKTTPFKDCKILRQRPRFVALKKQPSYIGGHESLE
LRDYQLNGLNWLAHSWCKGNSCILADEMGLGKTIQTISFMNYLFHEHQLYGPFLLVVP
                                                                                                                                                                                                                                                                                                                                                                            RKRYVIPCHTKAAHFDIDWCKEDDSNLLIGIYEYGYGSWEMIKMDPDLSLTQKILPDD
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/protein_id="AAD56024.1"
/db_xref="GI:5917756"
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Search completed: August 3, 2002, 02:12:57 Job time: 42547 sec

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Result
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10: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAT42754

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ABL32358
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Chick CHD-W gene f
Great tit CHD-W ge
Human secreted pro
Human immune syste
Human immune syste
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Chick CHD-1A gene
Chicken CHD-W gene
DNA encoding novel
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RESULTI

AMT42751

AMT42751

AMT4 AMT4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT42751;
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Human full-length	AAK94754	22	3379	0.4	25	5
Human kidney relat	AAI63356	22	2935	0.4	25	4
Human excretory re	90	22	2935	0.4	25	ū
Human secreted pro	AAF91890	22	2407	0.4	25	2
Human full-length	AAK94901	22	2228	0.4	25	Ξ
	0	20	2099	0.4	25	9
ecreted pr		21	1352	0.4	25	39
	AAV59280	19	1311	0.4	25	8
<u>a</u>	AAC81109	21	1300	0.4	25	37
sequence #		24	1177	0.4	25	6
secreted	AAF63808	22	1157	0.4	25	55
secreted	AAC74431	21	972	0.4	25	4
nervou	ABA15364	22	846	0.4	25	ü
dopsis t	AAC44102	21	770	0.4	25	2
	AAK82985	22	728	0.4	25	33
inflamm	AAH92867	22	700	0.4	25	õ
Human breast cance	AAL14263	22	693	0.4	25	9
ς.	AAL23125	22	596	0.4	25	8
Pax-6 co		21	550	0.4	25	27
_	AAC03813	21	423	0.4	25	96
_	AAS34304	22	414	0.4	25	55
Human polynucleoti	AAI92280	22	412	0.4	25	4
Human nervous syst	ABA11459	22	332	0.4	25	ï
lone FM37	AAV88585	20	331	0.4	25	22
	AAA42060	21	329	0.4	25	12
immune/hae	AAK58905	22	307	0.4	25	õ
CHD-1 ger	AAT42756	18	153	0.4	25	9
secreted		21	140	0.4	25	60
m	AAC13041	21	140	0.4	25	7
_	ABL34073	24	40862	0.4	26	9
Human gene regulat	116	24	5919	0.4	26	ភ
Human immune syste	ABL32732	24	5919	0.4	26	4
н	63	22	5919	0.4	26	ω
immune/haem	75	22	2785	0.4	26	2
gene expres	ω	20	300	0.4	26	H
Human immune syste	ABL33795		5474	0.4	27	0

ALIGNMENTS

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WPI; 1997-043127/04.
                                       Griffiths R, Tiwari B;
                                                                                                                            06-JUN-1995;
                                                                                                                                                                    05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                   Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                               (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                              12-DEC-1996.
                                                                                                                                                                                                                                                    WO9639505-A1.
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Matches
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aagactggcaaatgtcagggtcaggtcagtatcaggaactggttctgattctgaatcgg
         AAGACTGGCAAATGTCAGGGTCAGGGTCAGTATCAGGAACTGGTTCTGATTCTGAATCGG
                                                  GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAGCATAAAGATG
                                                                                                                      ctgagttttggaagtccagtccaagcatacttgctgtacagagatcagcagtgctcaaga
                                                                                                                                  CTGAGTTTTGGAAGTCCAGTCCAAGCATACTTGCTGTACAGAGATCAGCAGTGCTCAAGA
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                                       gtagtgaagattctgccgatgattcgtccagtgaaactaagaagaaaaagcataaagatg
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- used for sex determn. a)
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                   TGGGTCTGGGTAAAACAATACAAACAATTTCTTTTCTGAACTACCTGTTTCATGAACATC
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                                                                                         agcaaccatcttacattggaggacatgaaagtctggagttaagagattatcagttaaatg
                                                                                                   AGCAACCATCTTACATTGGAGGACATGAAAGTCTGGAGTTAAGAGAGATTATCAGTTAAATG
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agtticoctticoagagacttgatggatacataaaaggggaattgatgaggaagcactgg agtticoctticoagagacttgatggatacataaaaggggaattgatgaggaagcactgg arcartroaargcaagaagcarcaagagcartrotgrittractgctacaagaagcaagcactgg allillillillillillillillillillillillilli	GGÁACTAATCCTTCTTGACAAGCTACTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTTC		AAGAGCTTGAACCATTTTACTAAGAAGAGTTAAAAAAAGATGTAGAAAAGTCTTTACCTG 2340		TACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGGTGTCTCAATT	
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Db 38 Oy 38 Oy 39 Oy 39 Oy 39 Oy 39 Oy 39 Oy 39	Qy 366: Db 366 Qy 372 Db 372 Qy 378	Db 34 Qy 35 Db 35 Qy 36 Db 36				Db 28 Oy 29 Db 29 Db 30 Oy 30 Db 30
3781 aaagagagagtagaacttagaacttagaaagattagaacgttttcgaacttccagagatgc 3840 3841 AGGTGAAGACTAGTCATCTCTCACGAAGAAGATGCACCACTGCACAAATCCA 3900	P P P P	3481 gacgcagtaggagcagaagatattctggatctgatagtgactccatcacagaaagaa	CAMARIC CLAMC GENERAL GENERAL GENERAL CHARACEACH CHARACEACH CAMARIC CLAMC GENERAL GENERAL CLAMC GENERAL GENE	aggaaatggatataagatggaaatcttgaagctgaaactggggaaaatggggcaaatggtgcggaaatggagctgggaaatggggaaaatgagcaggtc CATTGACTGTAGGGGATGAGTTGCTTTCACAGGTTCAAGGTGGCGAACTTTTCCAATATGG [tgcatacaggttcaactccatcaagctctacacctttaataaagaagagttatcagcta TTTTGAAGTTTGGTGCTGAGGAACTCTTTAAAGAACCTGAAGGAGAAGAACAGGAGCCC	2881 cacagaatgatctgcaggcacaggcgagagctcatagaattggacagaagaaacaggtta 2940 2941 ATATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGA 3000

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Qy	4021	TGGCTATGGCAGCTGGGAAATGATAAAAATGGATCCAGATCTCAGCTTAACACAGAAG	0
Db	4021	gcagctgggaaatgataaaaatggatccagatctcagcttaa	1080
ρ ₀ γ	4081 4081	TTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACT 4	1140 1140
VΩ		CCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTG	20
Db	4141	.cctcattaaattactgaataaagaccttgcaagaaaggaagcacaaaggcttgctggt	1200
ρ ₀	4201 4201	CAGGCAATTCCAAGAGAAGGAAGAAGAAGAATAAGAATAAGATGAAGGCTTCAAAAA 4	1260 1260
, Q	4261	AAGAGTGATTCTTCACCACACCCTCAGAAAAATCTGATGAAGATG	. ω
č		аааадаадаасааадаусуастостовоодаадаадату	2
ρ γ	4321 4321	ATGAGGAGAGGATAACAAGGTAAATGAAATGTAAAATTTAAAA AATGAGAAGATAACAAGAAAATGTAAAA AATGAGAAGAGAGGAGGAGGATAACAAGGTAAATGAAATGAAATTTAAATTTAAAAAATGAAAATGAAAATGAAAATGAAAATTTAAAAAA	1380 1380
Qγ	4381	TTCCATTGCTGGATACTCCAGTTCATATTACTGCAACCAGTGAACCAGTTCCTATCT	44
Ъ	38	aaattccattgotggatactccagttcatattactgcaaccagtgaaccagttcctatct 4	1440
ρ Ογ	4441 4441	GAAGAACT gaagaact	1500
Qγ	4501	GGA	5
Ъ	Ü	tgtcaaagcagcactgaaacagctggatagaccagagaagggcctttctgaaagggag	1560
Оγ	4561 4561	AGCTGGAACATACTAGGCAGTGTCTAATCAAAATTGGGGATCACATTACAGAATGCCTGA 4	ത് ത
3 5	4621	AGGAGTACACAAATCCCGGAGCAAATAAAACAGTGGAGGAAAAATTTGTGGATTTTTGTGT 4	0891
δ	6	CAAGTTTACAGAATTTGATGCCAGAAAGCTGCACAAACTCTACAAACATGCAAT	74
В	4681	caagtttacagaatttgatgccagaaagctgcacaaactctacaaacatgcaatc	
Db Qy	4741 4741	rgacci tgacci	0081
Οy	4801	AGGAGACTACAAACC!	œ
В	_ ~	aatcagaaatccagatgtggaaagactgaaggagactacaaaccatgatgatagtagc	6
용 3	4861 4861	GGGACACTTATTCTCTCTGATAGACATTTATCACAATACCATGATCATCACCAAAGACAGGC 4 1 1 1 1 1 1 1 1 1	1920 1920
δ	4921	TCAGGGAGATGCTTACAAGAAAAGTGACTCCAGGAAAAGGCCATATTCAGCCTTCAGT	0861
Вb	4921	atcagggagatgcttacaagaaaagtgactccaggaaaaggccatattcagccttcagta 4	0861
Qy	98	GCAGATAC	5040
Db	98	tggaaaagatcacagagactgggatcactacaaacaggacagcagatactacagtgata	04
3 8	5041	GTAAACATAGAAAGTTAGATGACCACAGGAGCAGAAGCACAGGTCAAACCTGGAAGGAA	10
Ö	2	taaacatagaaagttagatgaccacaggagcagagaccacaggtcaaacctggaaggaa	ř

6240	GTAAAAATGGGGAAGGGAATATTTTATTCCATTTAGTGCTCCTTTTTTTATTGGATACTTT	هبو	Qy
6180	aaagtcagtatacttacatgttttaataaaatatctcgatggaatcagaa	6121	дb
6180	CTTTTCACAAAGTCAGTATACTTACATGTTTTAATAAAATATCTCGATGGAATC	\vdash	Qy
6120	aaatgagcttttttccgtcaggctttttttggctgttcctttccccaacaactcaggcct	6061	ДĎ
6120	ATGAGCTTTTTTCCGTCAGGCTTTTTTTTGGCTGTTCCTTTCCCCAACACTCAGGCC		Qy
90		0	Db
90	AATTAAAAAAATTTATATAAAATTAAAATTAAAATTAATTAATTAATTAAATTAATTAAATTAAAA	2	O ₄
00	ttctcctgttttgtgatcagttataatgcctttttatgaaacaaac	9	Db
9	TTCTCCTGTTTCTGATCAGTTATAATGCCTTTTTTATGAAACAAAC	Φ.	0
94		88	Db P
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88	aaggactttgttcacttttccaaagctacttgtttacattgtacaactgcgaccaccttgcc	00 (dd S
	atgtttcaggaaagaatgggggatttattttgttttatttcttggtagagaactct	0 6) Db
82	CTTATGTTTCAGGAAAGAATGGGGGATTTATTTTGTTTATTTCTTGGTAGAGAACTCTC	7	Оу
5760	tctaggctgaacacagattaaattatgtttgtaaatgaacacttaaacactgacctgt	7	Db
5760	TTCTAGGCTGAACACAGATTAAATTATGTTTGTAAATGAACACTTAAACACTGACCTGTG	7	Qy
5700	actgccctttcagactggatcttactataaaactctt		מם
5700	ACCTCAACACTGCCCCTTTCAGACTGGATCTTACTATAAAACTCTTCATGTCAAAGTG	6	Оу
5640	tgtgctgcaaatgttgtggcactttttttttaagaaatggaagatgtttacttttacagg		Db
5640	GTGCTGCAAATGTTGTGGCACTTTTTTTTTTTAAGAAATGGAAGATGTTTTACTTTTACAG	Ġ	Qy
5580	tycaagytctattatcccaacagaagaaaatatttttgtatttaaagtttatgctgcac	Ġ	dd
5580	GCAAGGTCTATTATCCCCAACAGAAGAAAAATATTTTTTGTATTTAAAGTTTATGCT	Ü	Qy
5520	gacttgaaagatatggactggatattctatcagtagcagtattgttacttctttccagga	4	Db
5520	ACTTGAAAGATATGGACTGGATATTCTATCAGTAGCAGTATTGTTACTTCTTTCCAGG	4	Qy
5460	cattttctggaccttctttttagccatatacagtaaactaacacagtaattgccttacat		Db
5460	ATTTTCTGGACCTTCTTTTAGCCATATACAGTAAACTAACACAGTAATTGCCTT	4	Qy
5400	cagatcacaaaagtacacctgaacatacatggagtagccggaagacataacaaagactga		Db
5400	AGATCACAAAAGTACACCTGAACATACATGGAGTAGCCGGAAGACATAACAAAGACTG	Ü	Оу
5340	agaggtctccttatggttcaagatctcccctaggacacagatctccatttgaacactcat	5281	Db
5340	GAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGAACAC1	Ñ	Qy
5280	actcagactggcaaatggaccacagagcttctggtagtggcccgaggtcaccactagatc		Дb
5280	CTCAGACTGGCAAATGGACCACAGAGCTTCTGGTAGTGGCCCGAGGTCACCACTAGAT	Ñ	Qy
5220	cagatcaccgttccacttcagaatacagccatcataaatcttcgagagattatagatacc	$\stackrel{\sim}{\vdash}$	Db
5220	AGATCACCGTTCCACTTCAGAATACAGCCATCATAAATCTTCGAGAGATTATAGATAC	\vdash	Qy
5160	acttaaaagacagccggggtcattcagatcaccgctcccattcagaccacaggatacact	5101	Дb
5160	CTTAAAAGACAGCCGGGGTCATTCAGATCACCGCTCCCATTCAGACCACAGGATACAC	5101	Qy

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Claim 8; Fig 3; 76pp; English
                                         Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                         WPI; 1997-043127/04.
P-PSDB; AAW08147.
                                                                                                                                                                   Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                                05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                               W09639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird; sex determination; chromodomain-Helicase-DNA binding 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino
                                                                                                                                                                                                                                                                                                                                                                                                                      and are ignored in the translated amino acid sequence given in Fig 3"
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                                                                           The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a constraint of the constant of the control the sex of progeny of a constant of the constant of the control the sex of progeny of a constant of the constant of the control the sex of progeny of a constant of the constant of the control the sex of progeny of a constant of the control the sex of progeny of a constant of the control the sex of progeny of a constant of the control the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT42754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT42754 standard; cDNA; 1316 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 caagaaaccccaggcaaagcagctacagacccgtgcagactacctcattaaattactgaa 110
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 Mismatches

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Pred. No. 1.7e-35;
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Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other

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DB 23;

Length 4222;

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                                       CC polypertide (II) sequences: (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynuclectides are also used in diagnostics as expressed sequence tags (for identifying expressed genes. (I) is useful in gene therapy techniques (I) restore normal activity of (II) or to treat disease states involving (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II), (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, gene mapping, identification of mutations or responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and cold sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 21771; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
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AAS85967 standard; cDNA; 4222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #21771.
Sequence 4222 BP; 1040 A; 1041 C; 883 G; 1258 T; 0 other;
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                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
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ilarity 100.0%;
Conservative
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2000US-0649167
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medical imaging; diagnostic; genetic disorder;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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6.3e-16;
ches 0;
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             4140 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAAGGAACCACA 4186
                                                                                                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
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birds - used for sex determn. and to control sex of process
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                                                                                                                                          Sequence 153
                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffiths R,
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DB; AAW08148.
tacctcattaaattactgaataaagaccttgcaagaaaggaagcaca
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                                                                                                                                                                                                                                                                                                                                                for sex determn. and
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                                                                                                                                           56 A; 36 C;
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                                                                                          Score 47;
                                                                                                                                           31 G; 30 T;
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                                                                             DB 18;
1.5e-10;
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                                                                                                                                           0 other;
                                                                                          Length 153;
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amino
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                          Human secreted protein 5' EST, SEQ ID NO: 10365.
                                                     06-OCT-2000
                                                                                                        AAC06290 standard; cDNA; 212 BP
                                                                                                                                                                                                                                                                                                Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997 (first entry)
                                                                                                                                                                         91 tacctcattaaattactgaataaagaccttgcaagaaa 128
                                                                                                                                                                                                                                           Local
                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1997-043127/04.
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                Conservative
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-GB01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome;
                                                                                                                                                                                                                                          0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                          Score 38; DB 18;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                               0;
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E

WO200200928-A2

Homo sapiens.

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RESULT 8
ABL323
XX
AC ABL323
XX
AC ABL323
XX
C6-MAR
XX
DE Human
XX
KW Human;
KW Human;
KW acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerolic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6463 TGGGCAATAATGTCAAATGTGCTATGCAGC 6492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain pustram regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. NO ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL32358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 212 BP; 72 A; 41 C; 32 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 10365; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033401-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL32358 standard; DNA; 6237 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; Pues 30; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 tgggcaataatgtcaaatgtgctatgcagc 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 21; Length 212; Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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RESULT 9
ABL33370/c
ID ABL333
XX ABL333
XX ABL333
XX Human;
AC ABL333
XX Human;
KW Human;
KW antiar
KW antiir
KW ACUTE
KW ACUTE
KW Gene;
XX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; a acute myeloid leukaemia; Alzheimer's disease; AIDS; epilep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5979 AAACAAACAAACAAACAAAAAAAAAAATTAAA 6008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002
                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                            neurofibromatosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL33370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL33370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                    03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2795 AAACAAACAAACAAAAAAAAACAATTAAA 2766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-)
                                                                                                                                                   02-JUL-2001;
                                                                                                                                                                                                                                                     WO200200928-A2
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                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system disease; cytosine methylation; teriosclerotic; antianaemic; cytostatic; nooti
                         EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 331; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000DE-1032529
2000DE-1043826
                                                                        2000DE-1032529
2000DE-1043826
                                                                                                                                                   2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1614 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3283 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      ease; AIDS;
psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                            bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                          anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated
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RESULT 1
ABL33795/
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                 Nucleic acid comprising for diagnosis and treatucytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid compris
for diagnosis and tracytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek
                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                antiinflammatory; cancer; eye disease; arteriosclerosis;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epile
                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                             02-JUL-2001;
                                                                                                                                                                                                                                         03-JAN-2002
                                                                                                                                                                                                                                                                  WO200200928-A2
                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                   neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                           antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL33795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL33795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6191 BP; 1678 A; 92 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                              (EPIG-)
                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACAAACAAACAAACAAAAAAAAAATTAA 6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAAACAAACAAACAAAAAAAAACAATTAA
                                                                                                                                              EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 5474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1343; 32pp + Sequence Listing;
                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           system associated gene SEQ ID NO: 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising fragment of chemically modified s and treatment of diseases associated with
                                                                                                                                                                       2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                              2001WO-EP07537
                                                  treatment
                                                                                                                                             AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                fragment of chemically modified nent of diseases associated with
                                                                                                                   Berlin
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 2824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
0.014;
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abnormal
                                                  abnormal
                                                             gene, useful
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                                                                                                                                                                                                                                                                                                                                                             anaemia;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammallan cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; senetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                  Claim 1; Page 849; 2479pp; English.
                                                                                                                                                                                                 Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                          WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                         Crkvenjakov R, Dickson M, Drmanac R, Drmanac S
Escobedo J, García PD, García V, Giese K, Inn
Jones WL, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ13346 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%;
1 Similarity 100.0%;
27; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US01619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA; 300 BP
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Pred. No.
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. 0.11;
                                                                                                                                                                                                                                                                                                                                                             Drmanac S;
                                                                                                                                                                                                                                                                                                                           Labat I
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                                                                                                                                                                                                                                                                                                                                              Innis MA;
                                                                                                                                                                                                                                                                                                          Reinhard C;
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Query Match
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Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK75594 standard; DNA; 2785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune; haematopoietic; immune/haematopoietic antigen; cancer;
itic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; vaccine;
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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleat acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic concerns and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoietic antigen genomic concerns and polynucleotides may be used to prevent. AAK64703 cc ancers and cancer metastases of haematopoietic antigen genomic concerns and polynucleotides may be used to prevent invention. AAK54950 and AAM82169 cc represent sequences used in the exemplification of the present invention.
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
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11 - NOV - 2000
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis
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                                                                        2785 BP;
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2000US-0246611
2000US-0246613
2000US-0249207
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2000US-0249210
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2000US-0249211
2000US-0249212
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2000US-0249265
2000US-0249265
2000US-0251030
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2000US-0251185
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2000US-02511868
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      0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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      Score ?
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26;
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      DB 22;
0.32;
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                                                                        0 other;
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                      Length 2785;
                                                                                                        present invention
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14-AUG-2000
14-AUG-2000
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22-AUG-2000
22-AUG-2000
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21-SEP-2000
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2000US -0225447 2000US -0225759 2000US -0225759 2000US -0226811 2000US -022681 2000US -022681 2000US -022681 2000US -022934 2000US -022934 2000US -022934 2000US -022934 2000US -022934 2000US -022951 2000US -022951 2000US -022951 2000US -022951 2000US -022951 2000US -023124 2000US -02313 2000US -02318 2000US -0234647 2000US -0246476 2000US -0246476 2000US -0246478 2000US -0246523 2000US -0246523 2000US -0246523 2000US -0246523 2000US -0246523

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RESULT 13
AAS46349/c
                                                                                                                                                                                                                                    The invention relates to a nucleic acid comprising a sequence of 18 cc bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC blaulphite, of genes associated with tumour suppression and concegenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a pertide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may cc form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for carreary for analysing diseases or the predisposition to specific condored therapy of existing diseases or the predisposition to specific cd diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the compared to another set of genetic and/or prognosis events which cc are disadvantageous to patients. The present sequence is one of the concorners.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
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06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS46349 standard; DNA; 5919 BP
Sequence 5919 BP; 1421 A; 69 C; 1641 G; 2788
                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 71; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-602752/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour suppressor gene derived chemically modified sequence #71.
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                                                                      ftp.wipo.int/pub/published_pct_sequences.
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T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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3118 AAACAAACAAACAAACAAAAAAACAAT

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RESULT 14
ABL32732/c
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                                                       Matches
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                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheiner's disease, AlDs, epilepsy, neurofibromatosis, rheumatoid_arthritis, psoriasis and inflammatory/ulcerative bowel
5979 AAACAAACAAACAAACAAAAAAAACAAT 6004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL32732;
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                                                                                                                                                                                            Sequence 5919 BP; 1421 A; 69 C; 1641 G; 2788 T; 0 other;
                                                                                                                                                                                                                                                   diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 705; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                 Similarity
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                                                                             0.4%; Score 26;
100.0%; Pred. No.
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100.0%; Pred. No.
Live 0; Mismatc
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). 0.31;
                                                                             DB 24;
0.31;
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                                                                                                       Length 5919;
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RESULT 15
AAS6118/C
ID AAS611
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XX Human
DT 29-JAN
CC AAF
PR WO2001
XX 18-OCT
XX 06-APF
PR 07-APF
PR 01-SEE
XX 16-APF
PR 01-SEE
XX 16-APF
CC Seclet
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CC ASSOC
CC 
                                                                                                                                                                                                                                                 The invention relates to 224 nucleic acid sequences comprising at least CC 18 bases of a chemically pretreated gene associated with gene regulation CC selected from 43 known genes (or complementary sequences). The CC chemical pretreatment converts cytosine bases unmethylated at the CC 5-position to uracil or another base with hybridisation behaviour CC dissimilar to cytosine, to enable analysis of cytosine methylations. CC The DNA sequences, oligomers (or sets/arrays) and method are CC useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by CC enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac CC disorders, haemophilia, solid tumours and cancer, Werner syndrome, CC esquence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this specification and is cascociated with the human gene regulation-associated genes.

CC of the printed specification, but was obtained in electronic format directly from WIPO at
Query Match
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Matches 26
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; Inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene regulation-associated gene oligonucleotide #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS61168 standard; DNA; 5919
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                                                                                                                                                                    Sequence 5919
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ch 0.4%; Score 26; Similarity 100.0%; Pred. No. 26; Conservative 0; Mismatch
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; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                    ВP;
                                                                                                                                                             1421 A; 69
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Page 13

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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BM486590 pgm2n.pk0
BM491730 pgp2n.pk0
BB479798 164616 BA
AW075773 xx85c01 x
AA824571 cc78hl1.s
AA480460 ne70d08.s
H80753 yv78d12.s1
AA483709 ne75g04.s
H99736 yx27g03.s1
H99724 yx27e03.s1
H99724 yx27e03.s1
AW591975 hf36e06 x
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AA60997 af09h02.s
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AA885644 oj32c04	×			63	11
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BI794545 ic91e08.y	.0 В1794545			66	38
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AA116690 mn28f07	9 AA116690		.0	66	36
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9	.0 BG071866	164 1	1.0 3	66	34
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AA943664 EST19916	_			67	30
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171	⊳			67	26
7	.0 BF559370		.0	67	25
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				79	23
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BG391166 60241718				82	21
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BE973688 60168	.0 вЕ973688			82	19
AI298448 qm90a12	M1430440			20	La

ALIGNMENTS

/organism="Gallus gallus" /strain="Commercial broiler and Ottawa Res. Centre strains 90 & 21" /db_xref="taxon:9031" /clone="pgm2n.pk002.b16" /clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth plate cDNA library (pgm2n)" /sex="Male and Female" /tissue.type="Breast muscle, leg muscle and epiphyseal growth plate"	
	FEATURES Source
University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-35 Fax: 302-831-2822 Email: cogburneudel.edu, www.chickest.udel.edu.	
EPIPNYSSAL GROWTH PIATE CDNA LIBRARY, USDA/IFAFS ANIMAL GENOME PROJECT Unpublished (2002) Contact: Larry A. Cogburn	JOURNAL COMMENT
	REFERENCE AUTHORS TITLE
Callus yallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	ORGANISM
EST. Chicken. Callus callus	KEYWORDS SOURCE
gallus), mRNA sequence. BM486590 BM486590.1 GI:18607520	ACCESSION VERSION
Epiphyseal Growth Plate CDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk002.bl6 5' similar to gb Ax650282.1 (Ar004397) chromo-helloase-DNA-bliding on the Z chromosome protein (Gallus	
BM486590 597 bp mRNA linear EST 07-FEB-2002 pgm2n.pk002.bl6 Normalized Chicken Breast Muscle, Leg Muscle, and	LOCUS DEFINITION
	RESULT 1 BM486590

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RESULT
BM491730
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                                                                                                  Gallus gallus
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
Phasianinae; Gallus.
                                                           chicken.
                                                                                  BM491730.1
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126 c 106 g 179 t
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/lab_host="E. coli EMDH10B"
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                                                                                                            AACTAGTAGAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAAACGATTAAA
                                                                                                                                                                              GCAAAGAGAGATTCAAACTTGGGCTCCTCAGATGAATGCTGTAGTTTACTTAGGAGATAT
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TCTCAAT
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                                GTTTAACATACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGG
                                                                                             AACTAGTAGAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAACGATTAAA
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Townsend Hall, Newark, DE
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library, USDA/IFAFS
Unpublished (2002)
Contact: Larry A. Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porter,T.E. and Cogburn,L.A. ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal library, USDA/IFAFS Animal Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. coli EMDH10B"
/note="Vector: pCMVSPORT6; Library made from pools of total RNA isolated from each tissue ages. Single pass sequencing from 5'-end" a 116 c 127 g 190 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pituitary/Hypothalamus/Pineal Library (pgp2n)"
/sex="Male and Female"
/tissue_type="pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Commercial broiler
/db_xref="taxon:9031"
/clone="pgp2n.pk007.e18"
/clone_lib="Normalized Chick
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Pred. No. 2.9e-153;
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Best Local Similarity
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USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                    234 E xa85c01.x1 NCI_CGAP_CML1 Homo mRNA sequence.
AW075773
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Seg primer: ATTTAGGTGACACTATAG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                   sapiens
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llarity 100.0%; Pred. No. 3.3e-25;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pow SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

178 t
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Li
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Similarity 100.0%; Pred. No. 5.5e-23;
82; Conservative 0; Mismatches 0; Indels
CDNA Library Arrayed by: Greg Lennon, Ph.D.

BNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
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/clone=lib="NCI_CGAP_CMLI"
...
/clone_lib="NCI_CGAP_CMLI"
...
/clone_lib="NCI_CGAP_CMLI"
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/clone="Index = Not = 
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/db_xref="taxon:9606"
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           cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 280 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 296)
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Location/Qualifiers
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www-bio.linl.gov/bbrp/image/image.html
Insert Length: 1636 Std Error: 0.00
                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                            AA480460.1
                                                                                                                                                     Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="germinal center B cell"
/lab_host="DH10B"
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/clone="IMAGE:1355877"
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Pred. No.
stop:
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Homo sapiens cDNA clone IMAGE:909615, mRNA
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                                                                                                                                                                                                                                                         High quality sequence stops: 224
Source: IMAGE Consortium, LINL;
This clone is available royalty free through LINL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., F
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E.,
,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H80753 352 bp
yv78d12.s1 Soares melanocyte 2NbHM
IMAGE:248855 3', mRNA sequence.
                                                                                                                                                                                                                                           Seq primer: Promega -21ml3
                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                     High quality sequence stop: 224.
                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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/tissue_type="melanocyte"
/tissue_type="melanocyte"
/lab_host="bettor: pT773D (Pharmacia) with a modified
/note="vector: pT773D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st st)
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/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
                                                                           /clone_lib="Soares melanocyte
/sex="Male"
                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:248855"
                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:3866561"
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1 Similarity 100.0%; I 82; Conservative 0;
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.lln1.gov/bbrp/lange/lmage.html
Seq primer: -41ml3 fwd.ET from Amersham.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA483709 354 bp mRNA linear EST 15-AUG-199; ne75g04.sl NCI_CGAP_Ewl Homo sapiens cDNA clone IMAGE:910134, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
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                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="TMAGE:910134"
/clone_lib="NCI_CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
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The WashU-Merck EST Project
Unpublished (1995)
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Fax: 314 286 1810
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/db_xref="GDB:3872638"
/db_xref="taxon:9606"
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High quality sequence stops: 360
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 929 Std Error: 0.00
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The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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                                                                                                                                                          Similarity
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314 286 1810
                                                                                                                                         Conservative
                                                                                                                                                                                                                                          double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned in the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." a 61 c 73 g 126 t 1 others
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:262972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:3872614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares melanocyte 2NbHM"
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Eutheria;
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Primates;
                                                                                                                                     Score 82; DB; Pred. No. 4.3
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                                                                                                                                     DB 10; I
4.3e-23;
hes 0;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                 CTTGAATATTTAAATTCTGTAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 419)
                                                                                                                                                         2w55h08.rl Soares_total_fetus_Nb2HF8_9w IMAGE:774015 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                numan
                                                                                                                                     AA442118.1
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a modified polylinker; Site_1: Not I; Site_2: Eco Rí; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M. Fatima Bonaldo.
53 c 77 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2933986"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                     GI:2153996
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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5. 4.3e-23;
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TITLE JOURNAL COMMENT

AUTHORS

FEATURES

source

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

21 (bases 1 to 434)
22 1 (bases 1 to 434)
23 Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marrin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Mite, Y., Wylie, T., Materston, R. and Wilson, R.

WashU-NCI human EST Project
WashU-NCI human EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3', mRNA sequence.
AA609977
AA609977.1 GI:2458405
EST.
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Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.lln1.gov) for further information.
Seq primer: -2Emi3 rev2 Ef from Amersham
High quality sequence stop: 372.
Location/Qualifiers
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Waterston,R. and Wilson,R.
Washn-Merck EST project 1997
Unpublished (1997)
Contact: Wilson RK
Washington university School of Medicine
4444 Forest Park Parkway, Box 8501, St., Louis, MO 63108
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434
af09h02.sl Soares_testis_NHT
3', mRNA secuence
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larity 100.0%;
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0; Mismatches 0;
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e IMAGE:1031187
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1 (bases 1 to 453)

2 (bases 1 to 453)

2 (bases 1 to 453)

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Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 971 Std Error: 0.00
Seg primer: -40013 fvd. Err from Amersham.
                     High quality sequence stops: 311 source: IMAGE Consortium, LIML priss clone is available royalty-free through LIML; contact the This clone is available royalty-free through LIML; contact the IMAGE Consortium (info@image.linl.gov) for further information. Seq primer: ml3 -40 forward seq primer: ml3 -40 forward high quality sequence stop: 311.
                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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yx37f09.s1 Soares melanocyte 2NbHM
IMAGE:263945 3', mRNA sequence.
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Homo sapiens cDNA clone
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REFERENCE AUTHORS

COMMENT

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RESULT 13 AA609977/c

KEYWORDS SOURCE

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Query Match Best Local S

Matches

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                             456 bp ou87h05.sl Soares NSF F8 9W_OT P IMAGE:1634841 3', mRNA sequence AI088006
                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                       1 (bases 1 to 456)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-*Torgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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thes 0;
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a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 33208-325895 Soares NbBF pool 1:
145032-147355, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF9-9W pool 1:
758280-760553, 772104-774407 Soares NbHFA pool 1:
758280-760553, 772104-774407 Soares NbHFA pool 1:
304776-30631, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 166 a 63 c 92 g 135 t
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Query Match
Query Match
1.2%; Score 82; DB 9; Length 456;
Best Local Similarity 10.0%; Pred. No. 4.1e-23;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy 5836 TTTCCAAAGCTACTTGTTTTACATTGTACACTGCGACCACCTTGCGCGCTTTTCATCACAAG 5895
Db 257 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCCTTTTCATCACAAG 198
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Search completed: August 2, 2002, 22:41:57 Job time: 30172 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
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Database length: 1873333701
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-HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
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6.9e-83 68
1.8e-70 26
0.0022 1
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1.20 1
1.41 15.81
1.54 15.85
10.84 17.56
39.24 21.58
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148.44 6.63
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51 | A.58643 Sequence 12 from patent
71 | A.58643 Sequence 13 from patent
71 | A.58643 Sequence 13 from patent
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AC09505 Homos sapiens chrome AC079515 Human chromosome 14 AL109605 Homos sapiens chrome AC07916 Homos sapiens chrome AC07966 Human chrome sapiens chrome AC07906 Homo sapiens chrome AC07916 Homo sapiens chrome AC087135 Mus musculus clone
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AUTHORS
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TOURNAL
MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-MAY-1997) Zoology, Molecular Lab,
Glasgow G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves; Neognathae; Phasianinae; Gallus.
1 (bases 1 to 6872)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene-"CHD-Z"
/function-"role in chromatin architecture"
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/codon_start-1
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228. .5654
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1. .6872
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1. .6872
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Neognathae; Galliformes; Phasianidae;
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0221 | AC102955 Rattus norvegicu
8216 | AC006875 Caenorhabditis
3 | 256422 H sapiens CpG island
1 | AX186475 Sequence 2370 from
4 | AX18747 Sequence 3342 from
7 | AX18747 Sequence 465 from P
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US-08-973-363-11 x AF004397
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LOCUS A58693
DEFINITION Sequence 12
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                          265 bp
Sequence 12 from Patent W09639505.
A58693.1 GI:3714251
                                                                                                                                                1 (bases 1 to 265)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                            unidentified
                                                                                                                                                                                                                         unidentified
                                                                 ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
                                                                                                                  Patent: WO 9639505-A 12 12-DEC-1996;
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THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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/note="short insert found
1223 c 1520 g 1683
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LOCUS A58694
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Sequence 13 from Patent W09639505.
A58694
                                                                                                          Quality:
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                                                                                                                        unidentified unidentified
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164144 bp DNA linear Homo sapiens clone RP11-1J4, WORKING DRAFT SEQUENCE,
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 164144)
Birren,B., Linton,L., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 13664 bases at least 040 consensus quality: 14722 bases at least 020 consensus quality: 152549 bases at least 020 consensus quality: 152549 bases at least 020 consensus quality: 152549 bases at least 020 linsert size: 17300; agarose-fp guality coverage: 3.1 in 020 bases; squarose-fp quality coverage: 3.1 in 020 bases; sum-of-contigs
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                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
1085 1184: contig of 1084 bp in length
1085 1184: gap of 100 bp
1185 2467: contig of 1283 bp in length
2468 2567: gap of 100 bp
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E, 47 unordered
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80241 84278:
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          94501 94600: gap of 100 bp
94601 99471: contig of 4871 bp in length
99472 99571: gap of 100 bp
99572 104300: contig of 4729 bp in length
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30150 31707: contig of
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1571: gap of 100 bp
104300: contig of 4729 bp in length
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                                                                                                                                                                                                                                                                            278: gap of 
89364: contig of
                                                                                                                                                                                                                                                                                                                                                            84178: contig of 3938 bp in length
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15920: contig of 1850 bp in length
20: gap of 100 bp
18236: contig of 2216 bp in length
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76509: contig of 3899 bp in length
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2: gap of 100 bp
5706: contig of 1424 bp in length
                                                                                                                                                                           gap of
)0: contig of
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alignment_block:
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Ratio: 1.000
Percent Similarity: 100.000
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misc_feature
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12122 121321; gap of 100 bp
121322 127038; contig of 5717 bp
127039 127138; gap of 100 bp
127039 133895; contig of 6757 bp
133896 133995; gap of 100 bp
133896 1340279; contig of 6284 bp
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104401 111387
111388 111487:
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116245 116344: gap of
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8876 .10671
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26071 ...27824
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5807. .7051
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2568. .4182
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/clone="RP11-1J4"
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31808. .33988
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27925. .30049
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12507. .13970
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                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="assembly_fragment"
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3: gap of
140279: cc
10370
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111387: cor
11487
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147004: contig of 6625 bp
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                                                                                                                             Percent Identity:
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grand-Pierre, N. Grant, G. Hagos, B. Heaford, A., Horton, L.,
Howland, J. C., Tilev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McDena, T., Miranda, C., McDenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                  * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-MAR-2000) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 3, 2000 this sequence version replaced gi:7670170. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,C., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 177957)
Birren, B., Linton, L.,
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Homo sapiens clone RP11-2N21, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                               Center project name: L2680

Center clone name: 2,N_21

Center clone name: 2,N_21

Center clone name: 2,N_21

Sequencing vector: M13; M77815; 100% of read Chemistry: Dye-terminator Big Dye; 100% of r Assembly program: Phrap; version 0.960731

Consensus quality: 174723 bases at least 040 Consensus quality: 17598 bases at least 040 Consensus quality: 177197 bases at least 020 Consensus quality: 177197 bases at least 020 Insert size: 182000; agarose-fp Insert size: 17557; sum-of-contigs Ouality coverage: 6.7 in 020 bases; agarose-Quality coverage: 6.8 in 020 bases; sum-of-contigs
This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: requence_submissions@genome.wi.mit.edu
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least Q30
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E, 5 unordered
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FEATURES

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alignment_block:
US-08-973-363-11 x AC025298
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    Quality:
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LOCUS ACD97
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DE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACU92372 101220 bp DNA linear PRI 07-DEC
Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
ACU92372
                             Direct Submission
Submitted (03-UUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USJ
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                Direct Submission
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DOE Joint Genome Institute.
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1829 1928: gap of 100 bp
1929 26417: contig of 24499 bp in length
26418 26517: gap of 100 bp
26518 54437: contig of 27920 bp in length
54438 54537: gap of 100 bp
5438 54537: gap of 100 bp
54538 101424: contig of 46887 bp in length
101425 101524: gap of 100 bp
101525 177957: contig of 76433 bp in length.
Location/Qualifiers
1. 177957
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101525. .177957
/note="assembly_fragment"
a 34244 c 35114 g 54995 t
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54538. .101424
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clone_end:SP6
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26518. .54437
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1929. .26417
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clone_end:T7
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/db_xref="taxon:9606"
/clone="RP11-2N21"
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US-08-973-363-11 x AC092372/rev
                                                                                                                                                 FEATURES
                                                                                                                                                                                          COMMENT
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LOCUS AC012624
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 LysGluLysArgGluAsnLysValLysGlu 76
                                                                                                                Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
1. .134365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USJ
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACU12624 134365 bp DNA linear PRI 21-JUL-
Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-shgc.stanford.edu pailty >=40 100% of Sequence; Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                           4 (bases 1 to 134365) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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AC012624.6 GI:14993679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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18862 c 17827 g 30409 t
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/db_xref="taxon:9606"
/chromosome="5"
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to: 101220

linear

PRI 21-JUL-2001

BASE COUNT ORIGIN

SOURCE ORGANISM

DEFINITION ACCESSION KEYWORDS ERSION

REFERENCE

AUTHORS TITLE

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JOURNAL TITLE AUTHORS JOURNAL

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LOCUS AC021449
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Quality:
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Boguslawkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
McGhand, J., Marquis, N., McSwan, P., McGurk, A., McKernan, K.,
Macdonald, P., Marquis, N., McSwan, P., McGurk, A., McKernan, K.,
McDheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Rova & Santos, B., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-58M12
Unpublished
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143079 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
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   Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
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                                                                                                                                                                 Center clone name: 58_M_12
                                                                                                                                                                                                 Center project name: L5154
                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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24497 c 25503 g 43951 t
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Quality: 10.00
Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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* NOTE: This is a 'working
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46906 47005: gap of 100 bp 107006 51830: contig of 4825 bp in length 51831 51930: gap of 100 bp 51931 62619: contig of 10689 bp in length 62620 62719: gap of 100 bp 62720 75408: contig of 12689 bp in length 75409 75508: gap of 100 bp 75509 92516: contig of 17008 bp in length 92517 92616: gap of 100 bp 1006409: contig of 13793 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases;
Quality coverage: 4.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 134743 bases at least Consensus quality: 139227 bases at least Consensus quality: 140814 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92617 106409: CULLY -- 100 bp 106410 106509: gap of 36570 t 106510 143079: Contig of 36570 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38820: contig of 38820 bp in length

38821 38920: gap of 100 bp

38921 40411: contig of 1491 bp in length

40412 40511: gap of 100 bp

40512 43279: contig of 2768 bp in length

4380 43379: gap of 100 bp

4380 43379: gap of 3526 bp in length
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106510...143079
/note="assembly_fragment
                                                                                                                                           /note="assembly_fragment"
92617. .106409
                                                                                                                                                                                                                                          /note="assembly_fragment"
62720. .75408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38921
                                              clone_end:T7
                                                                                                                                                                                                                                                                                         51931.
                                                                                                                                                                                                                                                                                                                                       47006
                                                                                                                                                                                                                                                                                                                                                                                     43380. .46905
                                                                                                                                                                                                                                                                                                                                                                                                                                 40512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11 Human Male
1. .38820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                               'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                          note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                  'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment"
ector_side:right"
26246 c 26678 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .143079
                                                                                                                                                                                                                                                                                         .62619
                                                                                                                                                                                                                                                                                                                                       .51830
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                                                                                                                                                                                            .92516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    draft' sequence.
    45278 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agarose-fp
    906 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q40
Q30
Q20
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Percent Identity:

100.000

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REFERENCE
AUTHORS
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AUTHORS
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US-08-973-363-11 x AC021449
FEATURES
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LOCUS AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_htg:AC008531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117867 AAAGAAAAAGAGAAAACAAAGTAAAAGAA 117896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q30
Consensus quality: 142744 bases at least Q30
Consensus quality: 142744 bases at least Q30
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* movided by the submittor.
       * This sequence will be replaced

* the finished sequence as soon as it is available and

* the accession number will be preserved.

* 56174 sound of 56174 bp in length

* 56175 56274 gap of unknown length

* 100875 100974 gap of unknown length

* 100875 100974 gap of unknown length

* 113128 113227 gap of unknown length

* 113128 113227 gap of unknown length

* 11328 113229 contig of 4963 bp in length

* 11329 118290 gap of unknown length

* 118291 118290 gap of unknown length

* 118291 119694 contig of 1404 bp in length

* 11995 123297 contig of 1404 bp in length

* 113298 123397 gap of unknown length

* 123298 123397 gap of unknown length

* 123298 123397 gap of unknown length

* 123298 123397 gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Direct Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Submitted (03-AUG-1999) Production Sequencing Facility, CA 94598, USA On Feb 14, 2001 this sequence version replaced g1:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145659 bp DNA linear HTG 14-FEB-2001
Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
7 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC008531.3 GI:12830078
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: CIT-HSPC_480B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center Project Name: 369535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 145659)
DOE Joint Genome Institute.
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REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AC091946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-973-363-11 x AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_htg:AC091946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AC008531 from: 1 to: 145659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48484 AAAGAAAAAAGAGAAAACAAAGTAAAAGAA 48513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LysGluLysArgGluAsnLysValLysGlu 76
                                         Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 18175 bases at least Q30
Consensus quality: 18175 bases at least Q30
Estimated insert size: 204590; agarose-fp estimation
Egatimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 33 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N. but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
** 1358. Contign of 1358 be in leasth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193446 bp DNA linear HTG 09-JUN-2001 Homo sapiens chromosome 5 clone RP11-360T2, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
AC091946
AC091946 GI:14333882
HTG; HTGS PHACE<sup>1</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
Center Project Name: 544799
Center clone name: RPCI-11_36012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing of Human Chromosome 5
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CTC-480B11"
/clone_lib="CalTech human BAC library C"
a 26309 c 27580 g 48609 t 600 other
1358: contig of 1358 bp in length 1458: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 100.000
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BASE COUNT
ORIGIN
                                                             FEATURES
                                                      source
        57571
                                                                     102895
110867
110967
117572
117672
117672
1123739
123839
123839
130584
130584
141645
141645
                                                                                                                                                                             92892
102795
                                                                                                                                                                                             87612
92792
                                                                                                                                                                                                             79896
87512
                                                                                                                                                                                                                            1. .193446
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chone="5p11-36012"
/clone="1b="RPCI human BAC library 11"
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                                                             Location/Qualifiers
                                                                                   102894: gap of unknown length
110866: contig of 7972 bp in ler
110966: gap of unknown length
117571: contig of 6605 bp in ler
117671: gap of unknown length
123738: contig of 6607 bp in ler
123838: gap of unknown length
130583: contig of 6745 bp in ler
130683: gap of unknown length
141544: gap of unknown length
141544: gap of unknown length
141644: gap of unknown length
1416459: contig of 10861 bp in ler
                                                                     169209: gap of unknown 193446: contig of 24237
                                                                                                                                                                                                                                                                                                                                   36065
36165
40978
                                                                                                                                                                                                                                                                                                                                                                                                                 18068:
20434:
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17968:
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16381
                                                                                                                                                                                   gap of contig
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                                                                                                                                                                                                         of unknown length
g of 10422 bp in length
of unknown length
g of 6151 bp in length
g of 6151 bp in length
of unknown length
of of 5563 bp in length
of unknown length
g of 7616 bp in length
of unknown length
of of 7616 bp in length
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                               alignment_block:
US-08-973-363-11 x AC026778/rev
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Quality:
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US-08-973-363-11 x AC091946
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
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Align seg 1/1 to reverse of: AC026778
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Homo sapiens chromosome 5 clone CTC-428I11, complete sequence.
AC026778
AC026778.4 GI:14277282
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Submitted (24 MAR-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459
3 (bases 1 to 195433)
DDE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 1, 2001 this sequence version replaced gi:13677045. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov
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DOE Joint Genome Institute
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SHGC-103595 G57841
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-428II1"
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LysGluLysArgGluAsnLysValLysGlu

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seq_documentation_block:
                                   seq_name: gb_htg:AC092382
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Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                           Quality:
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
ACU22121
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SHGC-103595 G57841
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
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DOE Joint Genome Institute.
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AC092382
AC092382.1 GI:14589571
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     276181 bp DNA
Homo sapiens chromosome 5 clone RP11-75H1,
47 unordered pieces.
AC093787
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 276181)
DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                         2 (bases 1 to 276181)
DOE Joint Genome Institute.
                                                                             Direct Submission
                                                                                                                                                           Jnpublished
                                                                                                                                                                                   Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear HTG 03-JUL-2001 WORKING DRAFT SEQUENCE,
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Project Information Center Project Name: 435334 Center clone name: RPCI-11_75H1

Consensus quality: 229677 bases at least 040
Consensus quality: 256163 bases at least 020
Consensus quality: 256163 bases at least 020
Consensus quality: 260799 bases at least 020
Estimated insert size: 174820; agarcse-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Ouality coverage: 8.62 in 020 bases; sum-of-contigs estimation
Ouality coverage: 8.55 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. Summary Statistics

1061: contig of 1061 bp in length
1161: gap of unknown length
2827: contig of 1666 bp in length
2927: gap of unknown length
4227: contig of 1300 bp in length
4327: gap of unknown length 8: gap of unknown length
4: contig of 1116 bp in length
6: contig of 1292 bp in length
6: contig of 1292 bp in length
0: contig of 1292 bp in length
0: contig of 1297 bp in length
7: gap of unknown length
7: gap of unknown length
7: gap of unknown length
0: contig of 1207 bp in length
1: contig of 1051 bp in length 7: gap of unknown length
7: contig of 1300 bp in length
7: gap of unknown length
8: contig of 1291 bp in length
8: gap of unknown length
8: contig of 1265 bp in length
9: contig of 1339 bp in length
10: contig of 1339 bp in length gap of contig gap of contig f unknown g of 1327 f unknown g of 1249 l bp in length n length 5 bp in length bp in length bp in length length

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                                                                                                                                                                                                                                            Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AC092382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                              AGAGAGAAGAAGAGAAGATAAA 631
                                                                                                ArgGluLysLysGluLysGluAspLys 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  720 bp mRNA linear PLN 02-1
Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
AL113980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY Cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1 to 720)

Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

Direct Submission
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Botryotinia fuckeliana.
Botryotinia fuckeliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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2 (bases 1 to 720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL113980.1 GI:5828599
                                                                                                                                                                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library was produced in an oriented direction,
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Botryotinia fuckeliana"
/strain="T4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      /note="Genoscope sequence ID : W25F061"
192 c 128 g 295 t
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Percent Identity:
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Gaps:
t Identity:
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Botryotinia.
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JOURNAL REFERENCE
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AUTHORS
                                                                                                                                                             BASE COUNT
ORIGIN
alignment_block:
US-08-973-363-11 x AB009080
                                                                                                        alignment_scores:
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DEFINITION
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                                      Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                polyA_site
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Direct Submission
Submitted (21-NOV-1997) Junichi Saito, University of Tokyo,
Submitted of Life Sciences, Graduate School of Arts & Sciences;
Department of Life Sciences, Graduate School of Arts & Sciences;
3-8-1, Komaba, Meguro-ku, Tokyo 153, Japan
3-8-1, Komaba, Meguro-ku, Tokyo ac.1p, Tel:+81-3-5454-6751,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (strain:AX2) DNA.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB009080 4875 bp DNA linear I
Dictyostelium discoideum gene for TRFA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:+81-3-5454-6751)
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J. Biol. Chem. (1998) In press
2 (bases 1 to 4875)
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Dictyostelium TRFA homologous to yeast Ssn6 is required for normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito, J., Adachi, H. and Sutoh, K.
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1 758 c 627 g 1327 t
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APIKPSSRKLER*
4875
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FENNSNNNNNNNNNNNNNNNNNNNNNNNNNNNNSSPERESSPEREILIDEESSEILERSSPERES
PSIYKEALEEKRETYIVDKERSPYPITTEKPODEGVEKVTPDKESSLVEKVDKENEKESP
SSSSSSKEIEKETEKEKEKEKEKEKEVEKEVEKEIENDKEKEKEKEKEVEKDVEENKSVE
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium discoideum"
/strain="AX2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA33143.1"
/db_xref="GI:3599670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(354. .1352,1489. .1581,1669. .2485,2596. .4859)
/gene="trfA"
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join(354. .1352,1489. .1581,1669. .2485,2596. .4859)
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                                  Length: 9
Gaps: 0
Percent Identity: 100.000
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Align seg 1/1 to: AB009080 from: 1 to: 4875

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Date: Aug 3, 2002 7:18 AM
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Database length: 858457221
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Query: US-08-973-363-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time (sec): 521.050000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MODEL-frame+_p2n.model -DEV-x1h
-Q-(cgn2_1/USPT0_spool/US08973363/runat_01082002_080123_19849/app_query.fasta_1.638
-DB-w_Geneseq_032802 -QFWT=fastap -SUFFIX=011p2n.rng
-GRPOP-4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=0.050 -MINMATCH=0.100 -YGAPOP=60.000
-XGAPEXY=60.000 -FGAPOP=6.000 -GAPEXT=7.000 -YGAPOP=60.000
-YGAPEXY=60.000 -DELDP=6.000 -DELEXT=7.000 -YGAPOP=60.000
-YGAPEXY=60.000 -DELDP=6.000 -DELEXT=7.000 -START 1
-MATRIX=011g0 -FRANS-human40.0d1 -LIST=45 -DOCALIGN=200
-THR_SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTEMT=pfs
-MORM-ext -HEAFSIZE=500 -MINLEN=0 -MAXLENEN-200000000
-USER-US0873353 =QCSU1_1 186 -NCPU=6 -ICPU=3 -LONGLOG
-USCRE-US0873353 =QCSU1_1 186 -NCPU=6 -ICPU=3 -LONGLOG
-USCRE-US0873353 =QCSU1_1 186 -NCPU=6 -ICPU=3 -LONGLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uery length: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of: US-08-973-363-11 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP=60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT=60.000
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      140.33 18.11
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0.0121
10.80
                          alignment_block:
US-08-973-363-11 x AAT42752
                                                                                                                         alignment_scores
     Align seg 1/1 to: AAT42752
                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT42752;
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                                                                   Quality:
Ratio:
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAX02996 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABLIS140 + /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAX02303 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAX03377 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAL03377 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAL03377 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAL03379 - /SIDS1/gcgdata/hold-geneseq/genes
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ID AAT42752 standard; cDNA; 265 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42752
                                                                                                                                                                                                                                                                                                                                                                                                A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                                                                                                                              Sequence 265 BP; 158 A; 16 C; 61 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 7; 76pp; English.
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misc_difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding l Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW08144.
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/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
in Fig 7"
     75.00
0.852
98.876
Length: 89
Gaps: 1
Percent Identity: 98.876
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                             A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif
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                                                                                The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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us-08-973-363-11 x AAH70996
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                                                              Percent Similarity: 100.000
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21-DEC-1999; 99US-0171350.
14-MAR-2000; 2000US-0189315.
12-MAY-2000; 2000US-0203791.
09-JUN-2000; 2000US-021660.
21-JUL-2000; 2000US-0220114.
                                                                                                                                                                                                                                       The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 480; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlegel R, Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000; 2000WO-US33312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cervical cancer marker nucleic acid 2270.
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                                                                                                                                                                                                Sequence 271 BP; 98 A; 56 C; 75 G; 41 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH70996 standard; cDNA; 271 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berger A, Zhao X;
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                  seq_documentation_block: ID ABA74794 standard.
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US-08-973-363-11 x ABA74794
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                                                                                     Align seg 1/1 to: ABA74794
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-00207456; 30-JUN-2000; 2000US-0608408; 03-AUG-2000; 2000US-0632366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0234535; 04-OCT-2000; 2000GB-0024263;
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. For this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 GAAGAAAAGCCAGAACCAGACATA 151
                                                                                                                                                                                                                                                                                                                               Sequence 287 BP; 139 A; 5 C; 138 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 23099; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #23099.
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16 AAAAGGGAGAAGAAGGAGAAGGAG 39
                    49 LysArgGluLysLysGluLysGlu 56
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Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID ABA39495 standard; DN
AC ABA39495;
XX ABA39495;
XX 23-JAN-2002 (first e
XX Probe #17961 for gene
XX Human; gene expressic
KW Human; gene expressic
KW Cardiovascular diseas
KW Cardiovascular diseas
KW Congenital heart diseas
XX O9-AUG-2001; 2001WO-U
XX 09-AUG-2001; 2000US-C
PR 03-JUN-2000; 2000US-C
PR 21-SEP-2000; 2000US-C
PR 03-JUN-2000; 2000US-C
PR 04-CCT-2000; 2000US-C
PR 05-MAY-2000; 2000US-C
PR 05-MAY-2000; 2000US-C
PR 03-JUN-2000; 2000US-C
PR 03-JUN-2000; 2000US-C
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PR 03-JUN-2000; 2000US-C
PR 04-CCT-2000; 2000US-C
PR 03-JUN-2000; 200
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                                                                                                                                                    US-08-973-363-11 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human heart present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derifrom the human heart via microarrays. By measuring gene expression, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular seg. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes measuring human gene expression in a sample derived from human h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease.
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                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA39495
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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ion, the
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seq_documentation_block:
ID AAK23286 standard; DN
XX
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XX O5-NOV-2001 (first e
XX Human brain expressed
XX Human; brain 2001Wo-10
XX Human; brain 2001Wo-1
XX Human; brain 2000WS-1
PR 30-JAN-2001; 2000WS-1
PR 21-SEP-2000; 2000WS-1
PR 21-SEP-2000
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US-08-973-363-11 x AAK23286
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    Quality:
                    seq_documentation_block:
                                                                      seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK49450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
AAK49450 standard; DNA;
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                                                                                                                       LysArgGluLysLysGluLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                          39
                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G;
                                                                                                                                                                                                                                                                                                                                                    Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                            287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
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100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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alignment_block:
US-08-973-363-11 x AAK49450
                                                                                       BX8X
                                                                                                                                                   seq_documentation_block:
ID AAI26561 standard;
                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI26561
                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAK49450
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO: 24007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001 (first entry)
            cervical cancer; ss.
                                                      Probe #16494 for gene expression analysis in human cervical cell sample.
                                                                                                                     AAI26561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 287 BP; 139 A; 5 C; 138 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                          Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                       12-OCT-2001 (first entry)
                                                                                                                                                 AAi26561 standard; DNA; 287 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO: 24007; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                       16 AAAAGGGAGAAGAAGGAG 39
                                                                                                                                                                                                                                          49 LysArgGluLysLysGluLysGlu 56
                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0236359.
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1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-08-973-363-11 x AAI26561
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI55319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAI26561 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0508408.
30-JUN-2000; 2000US-0508408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the valor int/pub/published_pct_sequences.
               WO200157272-A2
                                                                                 genetic disorder;
                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                  17-OCT-2001 (first entry)
                                                                                                                                                                                                      AAI55319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 287 BP; 139 A; 5 C; 138 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 16494; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                               Homo sapiens
                                                                                                                                 Probe #24005 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                      AAI55319 standard; DNA; 287 BP
                                                                                                                                                                                                                                                                                                                     16 AAAAGGGAGAAGAAGGAGAAGGAG
                                                                                                                                                                                                                                                                                                                                             49 LysArgGluLysLysGluLysGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 100.000
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity: 1
  alignment_block:
US-08-973-363-11 x
                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH72066
                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                 _documentation_block:
AAH72066 standard; cDNA;
08-DEC-1999;
21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                    Cervical cancer;
                                                                                                                                                                       Human cervical cancer marker
                                                                                                                                                                                                              AAH72066;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                            WO200142467-A2
                                                                                                                                Homo
                                                                                                                                                                                          19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                     08-DEC-2000;
                                                                                         14-JUN-2001
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                                                                                                                                                                                                                                                                                  16
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                                                                                                                                                                                                                                                                                           LysArgGluLysLysGluLysGlu 56
                                                                                                                                                                                                                                                                                  AAAAGGGAGAAGAAGGAGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic aczing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                        ç.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0633366.
; 2000US-0234687.
; 2000US-0236359.
 2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                                                                                                                                                                                                                                                                                                                                                                  вР;
                                                                     2000WO-US33312
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID No
                                       99US-0169681.
99US-0171350.
                                                                                                                                                                                                                                                                                                                                          AAI55319
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1.000
100.000
                                                                                                                                                                                                                                                                                                                        AAI55319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DK,
                                                                                                                                                   cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                  139 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24005; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 C;
                                                                                                                                                                                                                                 314
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                                                                                                                                                                                                                                                                                                                                                                        Percent
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                                                                                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                      nucleic acid 3340
                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                  39
                                                                                                                                                  pre-malignant condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
an placenta –
                                                                                                                                                                                                                                                                                                                                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                                        Identity:
                                                                                                                                                                                                                                                                                                                        ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Length:
Gaps:
                                                                                                                                                                                                                                                                                                                         287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes useful
                                                                                                                                                  gene therapy;
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAH69191
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                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-973-363-11 x
                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                             14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a per-malignant condition; to monitor the progression of cervical cancer or a pre-malignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                      08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                             19-SEP-2001
                                      Schlegel
                                                                                                                                                    08-DEC-2000;
                                                                                                                                                                         14-JUN-2001
                                                                                                                                                                                             WO200142467-A2
                                                                                                                                                                                                                                    Cervical cancer;
                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                     AAH69191 standard;
                                                                                                                                                                                                                                                                                                                                                                        104 GAAGAAAAGCCAGAACCAGACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                                                                                                                                                           20 GluGluLysProGluProAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid for diagnosing and treating cervical cancer
                                                                                                                                                                                                                                                         cervical cancer marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for gene
                                                          MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assessing and detecting compounds for treating the cancer
                                     æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                             2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                                                                                                                                                                                                             (first entry)
                                      Deeds
                                                                                                                                                    2000WO-US33312
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                                                                                                                      99US-0169681.
99US-0171350.
                                                                                                                                                                                                                                                                                                                                                                                                                AAH72066
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1.000
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy.
                                                                                                                                                                                                                                    cytostatic;
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                                     J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1051pp;
                                                                                                                                                                                                                                                                                                                      cDNA;
                                    Berger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                    pre-malignant condition;
                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                      ВР
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                                                          MEDICINE INC
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Gaps:
Identity:
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                                                                                                                                                                                                                                    gene therapy;
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isolated

nucleic

acid

for

diagnosing

and treating

cervical

cancer

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8×000000000x8
  seq_name:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal
                                                                                                                                   Penn
                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #10563.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 186; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and for assessing and detecting compounds for treating the cancer
measuring human gene expression in a sample derived from human roetal liver. The single exon nucleic acid probes may be used for predicting,
                                              Claim 1; SEQ ID NO 10563; 639pp + sequence listing; English.
                                                                                                           WPI; 2001-483447/52.
                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                               WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                            Human; foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA62258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA62258 standard; DNA; 575 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 357 BP; 125 A; 73 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:ABA62258
                                                                        genome-derived single exon nucleic acid probes useful for
ing gene expression in human fetal liver -
                                                                                                                                   Hanzel DK,
                                                                                                                                                                                 2000US-0180312
2000US-0207456
2000US-0508408
2000US-0632366
2000US-0632366
2000US-0234359
2000US-0236359
2000US-0236359
                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 G; 59 T; 8 other;
                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 8
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26-MAX-2000; 2000US-0207456.

30-UUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEB-2000; 2000US-0234687.

27-SEB-2000; 2000US-023659.

04-OCT-2000; 2000GB-0024263.
 measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
 Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
 Claim 1; SEQ ID NO 8070; 530pp; English.
 Single exon nucleic acid probes for analyzing gene expression in human
 WPI; 2001-488899/53.
 Penn SG,
 30-JAN-2001; 2001WO-US00666
 09-AUG-2001.
 Probe #8070 for gene expression analysis in human heart cell sample
 23-JAN-2002 (first entry)
 ABA29604;
 Sequence 575 BP; 223 A; 93 C; 188 G; 71 T; 0 other;
 (MOLE-) MOLECULAR DYNAMICS INC
 Homo sapiens.
 ABA29604 standard; DNA; 575 BP.
 49 LysArgGluLysLysGluLysGlu 56
 69 AAAAGGGAGAAGAAGGAGAAGGAG 92
 Quality:
 Hanzel DK,
 Ratio:
 1.000
 Chen W, Rank DR;
 Percent Identity: 100.000
 Ę.
```

e.g. cardiovascular disease, hypertension, cardiac arrhythmias congenital heart disease.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly f

part of the printed directly from WIPO

and

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 US-08-973-363-11 x ABA29604
 Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 at
 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
 Human brain expressed single exon probe SEQ ID NO:
 Sequence 575 BP;
 69
 49
 ftp.wipo.int/pub/published_pct_sequences.
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 223 A; 93
 10582; 650pp + Sequence Listing;
 probes
 from: 1
 Percent
 Ç
 188
 Rank DR;
 for analyzing
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Gaps: 0
Identity: 100.000
 <u>ن</u>
 ÷
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 other;
 gene expression in
 English
 human
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 Ratio:
 BP;
 AAK10591
 223 A;
 8.00
 93
 from: 1
 Percent
 c;
92
 56
 188
 <u>ი</u>
 ç:
 Identity:
 Length:
 71 T;
 575
 Gaps:
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 100.000
 other;
 0 &
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Database length: -1841457050
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DNA Sequencing by: Incyte Genomics, Inc.
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12066 row: g column: 08
High quality sequence stop: 674.
Location/Qualifiers
 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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 Email: d402hu@sakura.cc.tsukuba.ac.jp
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 Contact: Hideko Urushihara
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 University of Tsukuba
 Institute of Biological Sciences
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 JOURNAL
 TITLE
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 Email: generobielife.uiuc.edu
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This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Award in Functional Genomics to G.E. Whittfield.
 Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
 BB170001B10E08 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170001B10E08 5', mRNA sequence. B1508663
 An Expressed Sequence Tag
Behavior in the Honey Bee
Unpublished (2001)
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Fax: 217 244 3499
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Location/Qualifiers
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library avallability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Unpublished (1999)
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
 RPCI-23-120M12.TV RPCI-23 Mus musculus genomic clone RPCI-23-120M12 DNA sequence.
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 ,B., Levins
and Fraser,
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 Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P
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JOURNAL
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COMMENT

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Eukaryota: Mycetozoa: Dictyosteliida; Dictyostelium.
1 (bases 1 to 510)
Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi.M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental cDNA in Dictyostelium discoideum
Unpublished (1998)
 Plate: 120 row: M column: 12
Seg primer: T7
Class: BAC ends.
 Contact: Hideko Urushihara
 Dictyostelium discoideum.
 AU053344.1 GI:4701826
 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
 Institute of Biological Sciences
 d402hu@sakura.cc.tsukuba.ac.jp
T - Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
 /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/GJ mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 93 c
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/dev_stage="slug"
/dev_stage="slug"
64 c 63 g 120 t
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/strain="C57BL/6J"
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 Location/Qualifiers
 /clone_lib="RPCI-23"
 from: 1
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Percent Identity: 100.000
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 EST 28-APR-1999
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AUTHORS
 KEYWORDS
SOURCE
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US-08-973-363-11 x AW790096/rev
 BASE COUNT
ORIGIN
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US-08-973-363-11 x AU053344
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 alignment_scores:
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 DEFINITION
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Ratio: 1.000
Percent Similarity: 100.000
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 JOURNAL
 TITLE
 source
 307 AAAGAAGCTGAAGAAAAGAGAGAAACT 333
 31
 LysGluAlaGluGluLysArgGluThr 39
 AW790096 518 bp mRNA linear EST 01-MAY-2001 C01520-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone C01520 similar to 101 kd malaria antigen, mRNA sequence. AW790096
 Blumeria graminis f. sp. hordei.
Blumeria graminis f. sp. hordei
Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
1 (bases 1 to 518)
 RPCI-23-194A5.TJ RPCI-23
 Contact: Rasmussen, S.W.
Department of Yeast Genetics
 Unpublished (2000)
 expressed sequence tag analysis
 Gene identification in the fungal pathogen
 Thomas, S.W., Rasmussen, S.W., Glaring, M.A.,
 Carlsberg Laboratory
 AW790096.1 GI:13901693
 Email: swr@crc.dk
 131
 il. Carlsbergvej, DK-2500, Copenhagen, Denmark
45 3327 5230
45 3327 4766
 quality sequence stop:
 /organism="Blumeria graminis f. sp. h/db_xref="taxon:62688"
/clone="c01520"
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/cell_type="conidia"
/lab_host="Hordeum vulgare"
a 99 c 84 g 204 t
 Location/Qualifiers
 from:
 Gaps:
Percent Identity:
 Length: 9
Gaps: 0
Percent Identity: 100.000
 щ
542 bp DNA linear GSS 05-MAR-2001 Mus musculus genomic clone RPCI-23-194A5,
 ÷
 from:
 100.000
 ;
0:
 518
 Blumeria graminis by
 Rouster, J.A. and Oliver
 hordei"
 ACCESSION
VERSION
KEYWORDS
 ACCESSION
VERSION
 REFERENCE
AUTHORS
 SOURCE
ORGANISM
 seq_documentation_block:
LOCUS BF338481
 alignment_scores:
 BASE COUNT
ORIGIN
 FEATURES
 COMMENT
 SOURCE
 DEFINITION
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 Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
 JOURNAL
 TITLE
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 BF338481
 Seq primer: SP6
Class: BAC ends.
 and Fraser, C.M.
 AZ879168
 house mouse
 149
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alignment_block:
US-08-973-363-11 x AZ879168/rev
 Align seg 1/1 to reverse of: AZ879168
 522 GAGAAAGAGAACAAGAGAGAGCTAAAA 496
 41 GluLysGluAsnLysArgGluLeuLys 49
 Unpublished (1999)
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0200
Fax: 301 838 0208
 602034145F2 NCI_CGAP_Brn64
 Email: szhao@tlgr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 194 row: A column: 5
 Mus musculus
Eukaryota; Metazoa;
BF338481.1 GI:11284884
 Zhao, S., Nierman, W., Feldblyum, T.,
 Mouse BAC End Sequences from Library RPCI-23
 AZ879168.1 GI:13197234
 (bases 1 to 542)
 , mRNA sequence.
 Levins, M., Mcgann, S.,
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 84 g 212 t
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 Location/Qualifiers
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 Gaps:
Percent Identity:
 Chordata;
Rodentia;
 791
 191 bp
 Tsegaye, G., Geer, K., Krol, M.,
 from:
 Length:
 Craniata; Vertebrata;
Sciurognathi; Muridae;
 nRNA
sapiens
 Malek, J., Shatsman, S.,
 MD 20850, USA
 9
0
100.000
 to:
 linear EST 22-NOV-2000 cDNA clone IMAGE:4182227
 542
 Euteleostomi;
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REFERENCE AUTHORS

ORGANISM

COMMENT

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Ratio:
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US-08-973-363-11 x BF338481
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LOCUS BG533957
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Ratio: 1.000
Percent Similarity: 100.000
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 source
 52 LysLysGluLysGluAspLysLysGlu 60
 Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
Email: egapbs-remail.nih.gov
Tissue Procurement: CLONWECH Laboratories, Inc.
CDNA Library Preparation: CLONWECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 mRNA sequence
BG533957
 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLM94946 row: i column: 12 High quality sequence stop: 304.
 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 791).
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 602553058F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4662854 5',
 Homo sapiens
 Homo sapiens
 BG533957.1 GI:13525497
 Contact: Robert Strausberg, Ph.D.
 Unpublished (1999)
 /clone="IMAGE:4182227"
/clone_lib="NCI_CGAP_Brn64"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="gliboblastoma with EGFR amplification"
/lab_host="DHIOB (Tl phage-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 104 c 160 g 115 t
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/db_xref="taxon:9606"
 Location/Qualifiers
 Percent Identity: 100.000
 817 bp
 mRNA
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 EST 03-APR-2001
 REFERENCE
AUTHORS
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US-08-973-363-11 x BG533957
 FEATURES
 COMMENT
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 seq_name: gb_est2:BG612310
 ORIGIN
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 DEFINITION
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 KEYWORDS
 VERSION
 ACCESSION
 Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
 Align seg 1/1 to: BG533957 from: 1 to: 817
 TITLE
 ORGANISM
 JOURNAL
 source
 source
 63 GluLysAspAsnLysGluLysArgGlu 71
 Quality:
 High quality sequence stop: 565.
 BG612310.1 GI:13663681
 mRNA sequence
 numan.
 251
 1. .817
 Location/Qualifiers
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ORIGIN BASE COUNT FEATURES

REFERENCE AUTHORS

KEYWORDS SOURCE ACCESSION VERSION

ORGANISM

DEFINITION

```
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 817)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP
 http://image.llnl.gov
Plate: LLCM1464 row: c column: 15
High quality sequence stop: 730.
Location/Qualifiers
 BG61Z310 817 bp mRNA linear EST 18-APR-2001 602613632F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4739191 5',
 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLCM1609 row: p column: 08
 CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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//clone=_ilb="NAMGE_462854"
//clone=_ilb="NAMGE_4662854"
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//lab_host="phHOB [T] phage-resistant)"
//lab_host="phHOB [T] phage-resistant)"
//starongare | Still phage-resistant) |
//still phage-resistant) |
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 DEFINITION
 Quality: 9.00
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Percent Similarity: 100.000
 Align seg 1/1 to: BG612310
 ORGANISM
 JOURNAL
 AUTHORS
 source
 657 AAGGAGAGCACAAAAAAGAGAAAAGAG 683
 75 LysGluSerThrGlnLysGluLysGlu 83
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 BF161157 908 bp 601769402F1 NCI_CGAP_Lu29 Mus mu
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 http://image.llnl.gov
Plate: LLAM9197 row: d column: 02
High quality sequence stop: 620.
 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
 Mus musculus
 EST.
 mRNA sequence.
BF161157
 Contact: Robert Strausberg, Ph.D.
 Unpublished (1999)
 BF161157.1 GI:11041264
 nouse mouse.
 304
 Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 Colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Tibrary.
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith,
 Stem cell origin.
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/tissue_type="spontaneous tumor, metastatic to mammary.
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/clone="IMAGE:3988561"
 ocation/Qualifiers
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 /lab_host="DH10B (T1 phage-resistant)"
 184 c
 from: 1
 Percent
 194 g
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6
 Identity:
 Length:
 bp mRNA linear EST 30-OCT-2000 musculus cDNA clone IMAGE:3988561 5',
 Gaps:
 817
 135 t
 100.
 .
000
 be
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COMMENT

TITLE

SOURCE KEYWORDS VERSION

FEATURES

Percent Identity:

100.000

Gaps:

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KEYWORDS
SOURCE
ORGANISM
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 BASE COUNT
ORIGIN
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US-08-973-363-11 x BF161157/rev
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 alignment_scores:
 REFERENCE
 VERSION
 ACCESSION
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 ORIGIN
 BASE COUNT
 Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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Percent Similarity: 100.000
 TITLE
JOURNAL
 Align seg 1/1 to reverse of: BF161157
 AUTHORS
 source
 960
 39 ThrLysGluLysGluAsnLysArgGlu 47
 ACAAAGGAGAAGGAAAACAAGAGAGAG 834
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1140)
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 mRNA sequence.
 602507103F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4604160 5',
 Plate: LLCM1339 row: f column: 01 High quality sequence stop: 233.
 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Contact: Robert Strausberg, Ph.D.
 Unpublished (1999)
 Homo sapiens
 BG435095.1 GI:13341601
 CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (I
 520
 276
 a
 ω
 sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Avera'
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched
full-length clones and was constructed by CONTEN
 Library."
206 c
 Laboratories (Palo
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/lab_host="DH10B (T1 phage-resistant)"
 Location/Qualifiers
 186
 a
 Percent Identity:
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 180
 1140 bp
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 Alto, CA). Note: this is a
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 Length:
 Length:
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 266
 Gaps:
 73 t
 mRNA
 4
 9
0
100.000
 0.
 0 9
 linear
 EST 14-MAR-2001
 (LENE)
 Average
 for
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REFERENCE
AUTHORS
TITLE
 KEYWORDS
SOURCE
 ACCESSION
VERSION
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US-08-973-363-11 x BG537228
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US-08-973-363-11 x BG435095
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 1061 AAGAAAGAGGCAGAAGAGAGAGAA 1087
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 human.
Homo sapiens
 Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1149) 11 (bases 1 to 1149) 11 (bases 1 to 1140) 11 (bases 1
 BG537228 1149 bp mRNA linear EST 03-APR-2001 602565257F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4689711 5',
 http://image.llnl.gov
Plate: LLCM1506 row: b column: 16
High quality sequence stop: 255.
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BG537228
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 Contact: Robert Strausberg, Ph.D.
 504 a
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 from: 1
 from: 1
 Length: 9
Gaps: 0
Percent Identity: 100.000
 ţo:
 .
0
 1140
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TITLE
JOURNAL
REFERENCE
AUTHORS
 REFERENCE
AUTHORS
 alignment_block:
US-08-973-363-11 x AG178168/rev
 VERSION.
KEYWORDS
 alignment_scores:
 BASE COUNT
ORIGIN
 COMMENT
 DEFINITION
 seq_documentation_block:
 SOURCE
 ACCESSION
 Quality: 9.00
Ratio: 1.00
Percent Similarity: 100.000
 Align seg 1/1 to reverse of: AG178168
 TITLE
 ORGANISM
 JOURNAL
source
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsutumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911], Fax:81-45-503-910, Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
 sequence.
AG178168
AG178168.1 G1:16707848
AG178168.1 G1:16707848
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA,
Male BAC Library clone:RP43-050A23.T7.
Pan troglodytes
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
 AG178168 1310 bp DNA linear GSS 09
Pan troglodytes DNA, clone: RP43-050A23.T7, genomic survey
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Matanabo,H. and Sakaki,Y. Direct Submission
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 LIBRARY
 (bases 1 to 1310)
 Vector
R.Site 1
R.Site 2
 37
 Sequencing: T7
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/db_xref="taxon:9598"
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/csex="male"
/cell_type="lymphocytes"
/clone_lib="RPC1-43 Chimpanzee Male BAC Library"
1 448 c 371 g 436 t 18 others
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: EcoRI
 : ECORI.
 Length:
Gaps:
Percent Identity: 100.
 from:
 clone_lib:RPCI-43 Chimpanzee
 to: 1310
 . 000
 GSS 09-JAN-2002
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No.
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Maximum DB seq length: 200000000
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 Total number of hits satisfying chosen parameters:
 Word size :
 Searched:
 Scoring table:
 Run on:
 OM nucleic - nucleic search, using sw model
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Query
Score Match Length DB
 OLIGO_NUC
Gapop 60.0 , Gapext 60.0
 August 3, 2002, 02:12:57; Search time 10310.5 Seconds (without alignments) 537.850 Million cell updates/sec
 1797656 seqs, 10463268293 residues
 US-08-973-363-12
265
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
 GATGAGATTGTTTCAGTGAA.....AAGAAGTGAAGGAAGAGAAG 265
 dp_br:*
 em_pat:*
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A58693
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
 COMMENT
FEATURES
BASE COUNT
ORIGIN
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 JOURNAL
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 Patent: WO 9639505-A 12 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
 unclassified.

1 (bases 1 to 265)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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JOURNAL
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 ORGANISM
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 Griffiths,R. and Korn,R.M.

A CHD1 gene is Z chromosome linked Gene 197 (1-2), 225-229 (1997)
 Direct Submission Submitted (16-MAY-1997) Zoology,
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 Glasgow
 2 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
 Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae; Phasianinae; Gallus.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A.,
Barderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Banderson,S., Barna,T., Char,
 Eukaryota; Metazoa; Chordata; Cri
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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COMMENT

JOURNAL

Direct Submission

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JOURNAL
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AUTHORS
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 Huang, M.C., Idol, J., Lee-Lin, S.-Q., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., Morse, E., Ojodu, M.A., Pearson, R., Stantripop, S., Summers, T.J., Thomas, J.W., Thomas, P.J., Thomas, F.J., Walker, M.A., Wetherby, K.D. and Green, E.D.
 Submitted (29-APR-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
 Mus musculus chromosome 5 clone RP23-326E9 strain C57BL6/J, WORKING DRAFT SEQUENCE, 8 unordered pieces.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; l (bases 1 to 192079)
Beckstrom-Sterberg, S.M., Benjamin, B., Blakesley, R.W.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 Direct Submission
 Unpublished
 NISC Mouse Sequencing Initiative
 nouse mouse
 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
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Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
* consists of 9 contigs. The true order of the pieces
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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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 Mus musculus
 Mus musculus chi
DRAFT SEQUENCE,
 26; Conser
 Direct Submission
 Green, E.D.
 Unpublished
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
 AC068142.1 GI:7670126
 AC068142
 AC068142
 house mouse.
 NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces
 58560 a
 (bases 1 to 237405)
 HTGS_PHASE1; HTGS_DRAFT.
 Quality coverage: 7.28x in Q20 bases; Quality coverage: 6.20x in Q20 bases; Quality coverage: 6.50x in Q20 bases;
 Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.99319
Consensus quality: 230333 bases at least Q40
Consensus quality: 232224 bases at least Q30
Consensus quality: 232224 bases at least Q30
Consensus quality: 233239 bases at least Q20
Insert size: 212000; agarose-fp
Insert size: 237405; sum-of-contigs
 Center project name: yt
Center clone name: 053F18
Center clone name: 053F18
 Center: NIH Intramural Sequencing Center Center code: NISC
 Sequencing vector: plasmid; n/a; 100% of reads
 Contact: nisc_mouse@nhgri.nih.gov
 Web site: http://www.nisc.nih.gov
 Conservative
 ----- Project Information
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1 36452 c 35882 g 61161 t 24 others
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/chromosome="5"
 --- Genome Center
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 9
 unordered
 0;
 Score 26; Pred. No.
 237405 bp DNA linear HTG 29-APR-2000
le 5 clone RP23-53F18 strain C57BL6/J, WORKING
 Mismatches
 pieces.
 Craniata; Vertebrata; Sciurognathi; Muridae;
 DB 2;
0.14;
 0;
 Length 192079;
 sum-of-contigs
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 Euteleostomi;
; Murinae; Mus
 0;
 Gaps
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 32 AAAAAATAAAAACAGAAAAAAGAAAA 57
Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Salren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, M., Bastlen, V., BoguslavKiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferrelra, P., Fitthugh, W., Gage, D., Galagan, J., Gardyna, S., Goinde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagoo, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McBwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Minoga, V., Murphy, T., Naylor, J., Naylor, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 ACIU1977 52433 bp DNA linear HTG 23-NOV-2001
Mus musculus clone RP24-333M7, LOW-PASS SEQUENCE SAMPLING.
ACI01977
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 52433)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 HTG; HTGS_PHASEO.
 Birren,B., Linton,L., Nusbaum,C. and Lander,E. wins musculus, clone RP24-333M7
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 Inpublished
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gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 27758 bp in length
gap of unknown length
gap of unknown length
contig of 34466 bp in length
gap of unknown length
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gap of unknown length
145778: contig of 35343 bp in length
gap of unknown length
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 Score 26;
Pred. No.
 DB 2; Length 237405; 0.14;
 0; Indels
 0;
 Gaps
 COMMENT
 TITLE
 JOURNAL
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RESULT AC101977

LOCUS DEFINITION ACCESSION EYWORDS ERSION

BASE COUNT ORIGIN

Matches Query Match Best Local : FEATURES

source

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

SOURCE ORGANISM

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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
 * arbitrary Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will the preserved.
 * NOTE: This record contains 67 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigliio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 be preserved.
 937: gap of 100 bp 9237 9336; contig of 699 bp 9237 9336; gap of 100 bp 9337 9994; contig of 658 bp 9395 10094; gap of 100 bp 10095 10894; can of 700 bp 10795 10894; can of 700 bp
 2968: contig of 705 bp
2969 3068: gap of 100 bp
3069 3774: contig of 706 bp
3775 3874: gap of 100 bp
3875 4524: contig of 650 bp
4525 4524: gap of 100 bp
4625 4524: contig of 677°
5302 5401: contig of 677°
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 13246 1393
13932 14031: 14032 1470
 754: contig of 754 bp in length 755 854: gap of 100 bp 85 1486: contig of 622 1587
 10095 10794: contrag or 100 bp
10795 10894: gap of 100 bp
10895 11583: contrag of 689 bp
 6865 6964: yar
7634:
13932 14031: gap of 100 bp
14032 14703: contig of 672 bp in length
14704 14803: gap of 100 bp
14804 15467: contig of 664 bp in length
15468 15567: gap of 100 bp
16269: contig of 702 bp in length
16270 16369; gap of 100 bp
16370 17042: contig of 673 bp in length
 11584 11683: gap of 100 bp
11684 12362: contig of 679 b
 13146 13245:
 12363 12462:
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7735 8
 5302 5401:
 2164 2263:
 100 bp in length 100 bp in length 1586; gap of 100 bp 2163; contig of 632 bp in length 2263; gap of 277 hr 2968; ~
 6184:
 7634: contig of 670 bp in length
34: gap of 100 bp
8437: contio of 70 bp
 100 bp
6084 contig of 683 bp
4: gap of 100 bp
6864: contig of 680 bp
1: gap of 100
 13931: contig of 686 bp
 62: gap of 100 r
 6084:
 100 bp

6437: contig of 703 bp

100 sp

100 sp

100 sp

100 sp

100 sp

100 sp
 100 br
 100 bp
 bp in length
 bp in length
 bp in length
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Length

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100 bp
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 19501 19500: contig of 691 bp in 19501 19600: gap of 100 bp in 20277; contig of 677 bp in 20278 20377; gap of 100 bp 20378 21054: contig of 677 bp in 19601 20378 21054: contig of 677 bp in 1 21055 21154: gap of 100 bp 21155 21831; contig of 677 bp in 1 21832 21931; gap of 100 bp in 162623; contig of 691 bp in 163263 22722: gap of 100 bp 21932 2398: contig of 676 bp in 1en 3399 23498: gap of 100 bp 24212: contig of 676 bp in 1en 3399 23498: gap of 100 bp 24212: contig of 676 bp in 1en 24212:
 32052 33746: contig of 695 bb in le 32747 32846: gap of 100 bb in le 33550 33649: gap of 100 bb in le 33550 33649: gap of 100 bb in le 33550 33649: gap of 100 bb in le 3456 34455: gap of 100 bb in le 35170 35269: gap of 100 bb in le 35170 35269: gap of 100 bb in le 3520 36022: gap of 100 bb in le 3520 36022: gap of 100 bb in le 3520 36022: gap of 100 bb in le 36023 36707: contig of 685 bb in le 36023 36707: contig of 685 bb in le 36023 3791: contig of 684 bb in le 37492 37591: gap of 100 bb in le 39032: gap of 100 bb in le 39033: gap of 100 bb in le 39034 40743: gap of 100 bb in le 39034 40743: gap of 100 bb in le 39034 40743: gap of 100 bb in le 39036: gap of
43761 43860: gap of
43861 44557: contig of
44558 44657: gap of
44658 45283: contig of
45284 45383: gap of
 31952 32051:
 31153 31252:
 17945: ga
18709:
 100
18809: gap of
19500
 17142: gap of
17845: con
 2942: gap of 682 bp in length 2972: gap of 100 bp in length 30483: contig of 661 bp in length 30483: gap of 100 bp 31152: contig of 669 bp in length 31252: gap of 100 bp 31951: contig of 699 bp in length 32051: gap of 100 bp 31951: contig of 699 bp in length 32051: gap of 100 bp 31951: gap of 32746: contig of 695 bp in length
 077: gap of 100 bp
43760: contig of 683 bp
 contig
 0f
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of 697 bp in
 of
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 bp in
 bp in length
 'n
 in length
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TITLE
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TITLE
 SOURCE
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DEFINITION
 RESULT 7
AC092372/c
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 FEATURES
 FEATURES
 COMMENT
 VERSION
 KEYWORDS
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Best Local S
Matches 24
 JOURNAL
 JOURNAL
 TITLE
 JOURNAL
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 source
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 29
 ATAAAAAATAAAAACAGAAAAAA 52
 The numbe
 Homo sapiens chromosome
AC092372
AC092372.3 GI:17402768
 Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
 Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
 Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3_ (bases 1 to 101220)
 Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
1 (bases 1 to 101220)
DOE Joint Genome Institute and
 Finishing Completed at Stanford Human Genome
 Direct Submission
 2 (bases 1 to 101220)
DOE Joint Genome Insti
 Homo sapiens
 www-shgc.stanford.edu
 www.jgi.doe.gov
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Unpublished
 Direct Submission
 numan.
 h 9.1%; Score 24; DB Similarity 100.0%; Pred. No. 1. 24; Conservative 0; Mismatches
 49255 49354: gap of 100 bp 49355 50021: contig of 667 bp in le 50022 50121: gap of 100 bp 50122 50825: contig of 704 bp in le 50826 50925: gap of 100 bp 50926 51628: contig of 703 bp in le 51629 51728: gap of 100 bp 51729 52433: contig of 705 bp in le
 E: This insert is not the entire sequence of the clone (enti-
uence is 146.7kb). It is clipped at the overlap with AC012624
number of bases overlapped is 90404.
 45384
46090
46190
46861
46961
47689
 48568
 48468
 #0189: gap of 100 bp in 10
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 Location/Qualifiers
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 Institute.
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Stanford Human Genome Center.

2800 Mitchell

linear

PRI 07-DEC-2001

complete

DB 2 2;

Length 52433;

0;

Indels

0,

Gaps

0;

in in in in length Ħ

length length

length length length length

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ACCESSION
 RESULT
AC012624
LOCUS
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AUTHORS
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AUTHORS
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 BASE COUNT
ORIGIN
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AC021449
 Db 119928 AAAAGAAAAAGAGGATAAGAAAGA 119951
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 BASE COUNT
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 DEFINITION
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Best Local :
 JOURNAL
 JOURNAL
 JOURNAL
 JOURNAL
 AUTHORS
 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 watch 9.1%; Score 24; DB 9; Length 134365; Local Similarity 100.0%; Pred. No. 1.1; es 24; Conservative 0; Mismatches 0; Indels 0
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 Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
 Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 13435)
DOE Joint Genome Institute and Stanford Human Genome Center.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
 Homo saplens chromosome 5 clone CTD-2082I17, complete sequence. AC012624
AC012624.6 GI:14993679
 Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (Dases 1 to 13456)
DOE Joint Genome Institute and Stanford Human Genome Center.
 DOE Joint Genome Institute.
 Unpublished
 ACO21449 143079 bp DNA linear HTG 10-SEP-2000 Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
 Direct Submission
 Direct Submission
 AC012624
Homo sapiens
 ACO21449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT
 Direct Submission
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 (bases 1 to 134365)
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 Mismatches

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Pred. No.
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 PRI 21-JUL-2001
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 JOURNAL
REFERENCE
 REFERENCE
AUTHORS
TITLE
 COMMENT
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 AUTHORS
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearle, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacGonald, P., Marquis, N., WcEwan, P., McGurk, A., McKernan, K., MacGonald, P., Marquis, N., WcEwan, P., McGurk, A., McKernan, K., McCheeterson, R., Collear, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T., M., Peterson, K., Pierre, N., Fisani, C., Pollara, V., Raymond, C., Kiley, R., Rothman, D., Terrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and T.,
 Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://fry.genome.washington.edu/RM/RepeatMasker.html Genome Center
 * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143079)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Unpublished
 (bases 1 to 143079)
 Insert size: 144000; agarose-fp
Insert size: 142779; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
 Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 134743 bases at least Q40 consensus quality: 134743 bases at least Q20 consensus quality: 140814 bases at least Q20
 Center project name: 5
 Contact: sequence_submissions@enome.wi.mit.edu
----- project Information
Center project name: L5154
 Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seg.wi.mit.edu
 43280 43379: gap of 100 bp 43380 43379: gap of 100 bp 46380 47005: contig of 3526 bp in length 46906 47005: gap of 100 bp 47006 51830: contig of 4825 bp in length 51831 51930: gap of 100 bp 51931 62619: contig of 1068 bp in length 62620 62719: gap of 100 bp 62720 75408: contig of 12689 bp in length 62620 62719: gap of 12689 bp in length
 38820: contig of 38820 bp in length
38821 38920: gap of 100 bp
38821 40411: contig of 1491 bp in length
40412 40511: gap of 100 bp
40512 43279: contig of 2758 bp in length
62720 75408: con
75409 75508: gap of
 Submission
 and Zody, M.
```

```
ACCESSION
VERSION
KEYWORDS
 BASE CO
 RESULT 1
AC008531
 REFERENCE
AUTHORS
TITLE
 REFERENCE
AUTHORS
TITLE
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 SOURCE
 DEFINITION
 Db 117824 AAAAGAAAAAGAGGATAAGAAAGA 117847
 FEATURES
 COMMENT
 Locus
 Query Match
Best Local S
Matches 24
 ORGANISM
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 misc_feature
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 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 Direct Submission Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US On Feb 14, 2001 this sequence version replaced gi:7528342.
 1 (bases 1 to 145659)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 Homo sapiens chromosome
 2 (bases 1 to 145659)
DOE Joint Genome Institute.
 Homo sapiens
 AC008531.3 GI:12830078
HTG; HTGS_PHASE2; HTGS_DRAFT.
 AC008531
 Center:
 -----Genome Center
 namur
 Similarity
 ordered pieces.
 43971
 75509 92516: contig of 17008 bp in length
92517 92616: gap of 100 bp
92617 106409: contig of 13793 bp in length
106410 106509: gap of 100 bp
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 Conservative
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Joint Genome Institute
Code: JGI
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 Mismatches
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 Length 143079;
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 Indels
 HTG 14-FEB-2001
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 Gaps
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VERSION
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ORIGIN
 REFERENCE
 DEFINITION
 LOCUS
 Query Match
Best Local Similarity
 AUTHORS
 ORGANISM
 Matches
 source
 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 * the accession number will be preserved.

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56175 56274: gap of unknown length

100875 100874: contig of 44600 bp in length

100875 100974: gap of unknown length

110975 113127: contig of 12153 bp in length

113128 113127: gap of unknown length

113128 113129: gap of unknown length

118191 118290: gap of unknown length

118191 118290: gap of unknown length

118695 119794: gap of unknown length

119795 123297: contig of 3030 bp in length

119794: gap of unknown length

119795 123297: contig of 3030 bp in length

113298 123397: gap of unknown length

123298 123397: gap of unknown length

123398 123397: gap of unknown length
 AC092736
Trypanosoma
IN PROGRESS
 Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q30
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; punse field gel estimation
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
 1 (bases 1 to 145830)
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 Trypanosoma brucei
 AC092736
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 Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
Melville,S.,
 Trypanosoma.
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma brucei.
 HTG; HTGS_PHASE2
 AC092736.5 GI:15920106
 Summary Statistics
 Project Information
 Web site: http://www.jgi.doe.gov
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100.0%;
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Adams, M.D.,
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 DB 2;
Donelson, J.E. and
 BAC library C"
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 Length 145659;
 600 others
 Indels
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 Gaps
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REFERENCE AUTHORS TITLE

TITLE JOURNAL

COMMENT

FEATURES

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Oryza sativa
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 Published Only in DataBase (2001) In press 2 (bases 1 to 154157) SassKi,T., Matsumoto,T. and Yamamoto,K.
 Sasaki,T., Matsumoto,T. and Yamamoto,K.

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AC007934
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 Query Match
 Homo sapiens
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 Conservative
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JOURNAL TITLE

AUTHORS TITLE

COMMENT

VERSION KEYWORDS

ACCESSION DEFINITION

SOURCE

ORGANISM

RESULT 1 AP003509

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 Submitted (30-JUN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 157625)
 Homo sapiens, clone RP11-29A1, complete sequence. AC007934
 * the accession number will be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Mismatches
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| repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region                                                                                                                                                                                                          | repeat_region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | repeat_region<br>repeat_region<br>repeat_region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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AC091946
LOCUS
 COMMENT
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Best Local
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 ORGANISM
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Consensus quality: 180259 bases at least 020
Consensus quality: 180259 bases at least 020
Consensus quality: 1804175 bases at least 020
Estimated insert size: 20450; agarose-fp estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation.
**NOTE: This is a "working draft' sequence. It currently
**consists of 33 contigs. The true order of the places
**Is not known and their order in this sequence record is
**arbitrary. Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
**as soon as it is available and the accession number will
**be preserved.
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Sequencing of Human Chromosome 5
Unpublished
 Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
------Genome Center
Center: Joint Genome Institute
Center: Code: JGI
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Center Project Name: 544799
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 Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
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www.jgi.doe.gov
 Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
 Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 219258) BOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
AC022121
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/clone="CTD-2007H13"
/d a 42062 c 40933 g 64309 t
 Location/Qualifiers
1. .219258
 3, 2002, 02:15:42
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 4
 Length 219258;
 0
 Indels
 PRI 30-AUG-2001
 0;
 Gaps
 0;
```

9

```
Title:
Perfect score:
Sequence:
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 OM nucleic - nucleic search, using sw model
 Total number of hits satisfying chosen
 Word size
 Searched:
 Scoring table:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 Score
 N_Geneseq_032802:*

1: /SIDS1/gcgdata/hc
2: /SIDS1/gcgdata/hc
4: /SIDS1/gcgdata/hc
4: /SIDS1/gcgdata/hc
5: /SIDS1/gcgdata/hc
5: /SIDS1/gcgdata/hc
6: /SIDS1/gcgdata/h
7: /SIDS1/gcgdata/h
7: /SIDS1/gcgdata/h
9: /SIDS1/gcgdata/h
110: /SIDS1/gcgdata/h
12: /SIDS1/gcgdata/h
13: /SIDS1/gcgdata/h
13: /SIDS1/gcgdata/h
14: /SIDS1/gcgdata/h
15: /SIDS1/gcgdata/h
16: /SIDS1/gcgdata/h
17: /SIDS1/gcgdata/h
18: /SIDS1/gcgdata/h
19: /SIDS1/gcgdata/h
19: /SIDS1/gcgdata/h
19: /SIDS1/gcgdata/h
20: /SIDS1/gcgdata/h
23: /SIDS1/gcgdata/h
23: /SIDS1/gcgdata/h
23: /SIDS1/gcgdata/h
23: /SIDS1/gcgdata/h
24: /SIDS1/gcgdata/h
24: /SIDS1/gcgdata/h
 Query
Match
 1: \sidesigned \square \text{...} Listing first 45 summaries
 OLIGO_NUC , Gapop 60.0 ,
 1736436 seqs, 858457221 residues
 US-08-973-363-12
265
1 GATGAGATTGTTTCAGTGAA......AAGAAGTGAAGGAAGAAG 265
 August 3, 2002, 01:52:38;
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
 Length
 DB
 Gapext 60.0
 AAT42752
AAT42753
ABA21438
AAZ29250
AAZ29252
AAZ29252
AAZ29254
AAA70286
 parameters:
 Search time 949.74 Seconds
(without alignments)
479.060 Million cell updates/sec
 3472872
Chicken CHD-IA ins
Chicken CHD-W clon
Human nervous syst
Rifin 3192 gene.
Rifin 3194 gene.
Rifin 3198 gene.
Plasmodium falcipa
Plasmodium falcipa
 Description
 RESULT
AAT42752
ID AAT4
XX AAT4
XX AAT4
XX Chic
XX Chi
 000
 იი
 Key
misc_difference
 Bird; sex determination; chromodomain-Helicase-DNA binding 1 CHD-W; chromodomain-Helicase-DNA binding on the W chromosome;
 Chicken CHD-1A insert motif.
 06-JUN-1995;
 05-JUN-1996;
 Gallus
 12-MAR-1997
 AAT42752 standard; cDNA;
 (ISIS-) ISIS INNOVATION LTD
 12-DEC-1996.
 W09639505-A1
 AAT42752;
 sp.
 (first entry)
 95GB-0011439
 96WO-GB01341.
 Location/Qualifiers 52
 /*tag= a
/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
in Fig 7"
 6898
13792
15453
16217
111
231
358
361
384
390
 265
 ABL18816
AAIF41813
AAII44389
AAAZ92526
AAAA39551
AAAA790760
 ABL24206
AAS85158
ABL07762
AAS61223
AAS61223
ABL05298
ABL33571
AAF29339
ABL32624
AAI24442
AAI244720
AAI44720
AAI44720
AAI4471573
AAI71573
 ВP
 ALIGNMENTS
 Human recombinant
Human steroid rece
NER receptor poten
Drosophila melanog
DNA encoding novel
Drosophila melanog
Human gene regulat
Drosophila melanog
Human immune syste
Atopy related gene
Human secreted pro
Human secreted pro
Human secreted pro
Human cervical can
Human cervical can
Human cervical can
 Human colon cancer
Human polynucleoti
Human polynucleoti
Genomic sequence #
Nucleotide sequenc
Human cDNA clone (
 Drosophila melanog
Human polynuclecti
Probe #13075 used
Rifin 3201 gene.
Human colon cancer
Plasmodium falcipa
Retinoblastoma pro
Bacillus anthracis
 DNA encoding novel
Human cDNA sequenc
Nucleotide sequenc
```

Result

ŏ

```
Qy
 DЬ
 Ωy
 밁
 δÃ
 밁
 Qy
 밁
 PT DR XXX
 B
 δÃ
 Matches
 A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
 Disclosure;
 Gallus
 CHD-W;
 12-MAR-1997
 AAT42753
 Sequence
 AAT42753;
 12-DEC-1996
 WO9639505-A1.
 misc_difference
 241
 241
 181
 121
 181
 121
 61
 61
 r
 1 GATGAGATTGTTTCAGTGAAACATCTACATAAAAAAAATAAAAAACAGAAAAAAAGAAAATGA
 Ν
 1997-043127/04.
 agaaaaagaagtgaaggaagaag
 AGAAAAAGAAGTGAAGGAAGAAG 265
 gatgagattgtttcagtgaaacatctacataaaaaaataaaaaacagaaaaaatga
 attaaaagaaaaagataataaagaaaagagagaaaacaaagtaaaagaatccacacagaa
 ATTAAAAGAAAAAGATAATAAAGAAAAGAAAGAAAACAAAGTAAAAGAATCCACACAGAA
 AGAGAAGGAAAATAAAAGGGAATTGAAAAGGGAAGAAAAAGAAAAAGAGGATAAGAAAGA 180
 agaaaagcctgagccagatattggtataaagaaggaagctgaagaaaaaaagagagacaaa
 AGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAGAGAGACAAA
 sex
 chromodomain-helicase-DNA binding genes determine sex — used for sex determn. and to control sex of progeny
 chromodomain-Helicase-DNA binding on the
 CHD-W
 Similarity
 265
 standard;
 R,
 determination; chromodomain-Helicase-DNA binding
 Fig 7; 76pp;
 Conservative
 B₽;
 (first
 clone
 Tiwari
 Location/Qualifiers 52
 /note=
 /*tag≔
 158
 CDNA;
 entry)
 100.0%;
 A; 16
 B
 "base 52 disrupts the
the translated amino
in Fig 7"
 р
 ω
 137
 English.
 Ç;
 motif.
 ВP
 Pred.
 61 G;
 Score 265; DB 18;
Pred. No. 1.6e-101;
 265
 Mismatches
 30
 Τ;
 0 other;
 reading frame acid sequence
 0;
 Σ
 chromosome;
 Length
 Indels
 for
given
 1 Avian;
 0;
 in
 120
 60
 ç
 180
 120
 60
 0;
```

31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000;

2000US-0184664. 2000US-0186350.

2000US-0180628

2000US-0189874. 2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0209467. 2000US-0214886.

17-JAN-2001; 16-AUG-2001. WO200159063-A2

2001WO-US01334.

```
RESULT
 B
 Qy
 ABA21438/c
 Query Match
Best Local S
Matches 33
 There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product splicing. The motif is also found as an insert in some CHD-1 (see also AAT42752).
 A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW8145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif
 Avian
birds
 antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 Human; nootropic; neuroprotective; cytostatic; dermatological; vi immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vul antiparkinsonian; antistckling; antianaemic; antiarthritic; cance antiparkinsonian totickling; anticortive; antiarthritic; cance antirheumatic; antiarthritic; cerebroic; anti-participartics; anti-partical participartics; anti-particip
 neurological
 Sequence 137
 Disclosure;
 05-JUN-1996;
 Human nervous
 ABA21438;
 ABA21438
 (ISIS-) ISIS
 103
 103
 ω
 AGAAAAAGAGAGACAAAAGAGAAGGAAAATAA
 1997-043127/04
 agaaaaaagagagacaaaagagaaaggaaaataa
 chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
 . Similarity 33; Conser
 AAW08145
 standard;
 ₽,
 Fig 7; 76pp; English.
 Conservative
 BP;
 disease;
 (first entry)
 INNOVATION
 system related polynucleotide SEQ ID NO 13769.
 96WO-GB01341
 75
 DNA;
 Ą;
 100.0%;
 12.5%;
 infection; nephrotropic;
 10 C;
 393
 0;
 Score :
 34
 G;
 Mismatches
 . 33;
 18
 Τ.
 135
 135
 0.00011;
 DB 18;
 0 other;
 0;
 Length 137;
 some CHD-1A clones
 cancer;
 0;
 in
 of
 vulnerary;
 virucide;
```

0

-JUN-2000;

14 - AUG-14 - AUG-14 - AUG-14 - AUG-14 - AUG-14 - AUG-14 - AUG-

```
17-NOV-
17-NOV
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antipagonists are useful in the diagnosis, treatment and prevention of; (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone
 Nucleic acids encoding 3224 human useful for preventing, diagnosing cancers and metastases .
 WPI;
 Disclosure;
 (HUMA-)
 -NOV-20
-NOV-21
-NOV-20
-NOV-20
-NOV-20
-NOV-20
 -NOV-20
-NOV-20
-NOV-20
-NOV-20
-NOV-20
 VON
 2001-541565/60.
 CA,
 HUMAN
 Barash
 SEQ ID NO 13769; 1701pp + Sequence Listing; English.
 2000US-0241808

2000US-0241808

2000US-0241826

2000US-024627

2000US-0246476

2000US-0246477

2000US-0246477

2000US-0246528

2000US-0246528

2000US-0246528

2000US-0246528

2000US-0246528

2000US-0246610

2000US-0246610

2000US-0246610

2000US-0246611

2000US-0246611

2000US-0249209

2000US-0249211

2000US-0249216

2000US-0251160

2000US-02511869

 GENOME
 SC,
 SCI
 Ruben
 SM;
 nervous system antigen polypeptides, and/or treating nervous system
```

2000US-0215135 2000US-021647 2000US-0217487 2000US-0217487 2000US-022964 2000US-0225266 2000US-0225266 2000US-022575 2000US-022575 2000US-022577 2000US-022577 2000US-022577 2000US-022577 2000US-022575 2000US-0225747 2000US-022575 2000US-0225747 2000US-0225747 2000US-0225747 2000US-0225747 2000US-0225747 2000US-0225747 2000US-0225747 2000US-0235414 2000US-0235414 2000US-0235414 2000US-023593 2000US-023593 2000US-023593 2000US-023593 2000US-0235836 2000US-0236368 2000US-0236868 2000US

14 - AUG - 2000
14 - AUG - 2000
18 - AUG - 2000
18 - AUG - 2000
22 - AUG - 2000
23 - AUG - 2000
23 - AUG - 2000
21 - SEP - 2000
01 - SEP - 2000
05 - SEP - 2000
06 - SEP - 2000
07 - SEP - 2000
08 - SEP - 2000
09 - SEP - 2000
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01 - SEP - 2000
02 - SEP - 2000
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04 - SEP - 2000
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09 - SEP - 2000
01 - SEP - 2000
02 - SEP - 2000
03 - SEP - 2000
04 - SEP - 2000
05 - SEP - 2000
06 - SEP - 2000
07 - CCT - 2000

밁 20

```
RESULT
AAZ29250
ID AAZ2
XX AAZ2
AX AAZ2
XX Rifj
DT 28-F
XX Rifj
KW Stag
KW Manman
KW Stag
KW Anti
XX Plag
XX WO9
XX WO9
XX WO9
XX WO9
XX WO9
XX O4-I
XX US
PR 24-,
PR 23-,
YR US
PR US
PR US
XX WPI
XX US
PR US
PT Of
XX The
CC Stz
CC Stz
CC Pli
CC Pli
CC C Pli
CC C Id
CC Va
XX
 Matches
 Query Match
Best Local
 marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroidiltis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infectious.
 selected
purified
 WPI;
 Rifin 3192 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid VR1050; DNA vaccine; immunisation; stage specific protein expression; antimicrobial vaccine; antimicrobial drug; IAP; immunofluorescent antibody testing; ds
 Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
 Claim 12; Page 16; 23pp; English
 24-APR-1998;
23-APR-1999;
 04-NOV-1999
 Rifin 3192
 28-FEB-2000
 Hoffman
 26-APR-1999;
 W09955381-A1
 Plasmodium falciparum
 AAZ29250;
 AAZ29250 standard; DNA; 930
 Sequence 393
 stages
 (USNA)
 were
 The present sequence is the Rifin 3192 gene of chromosome
 391
 41 AAACAGAAAAAAAAAAATGAAGA 63
 e of microbial, animal and/or human genomic data for identification
vaccine, drug or diagnostic products -
 4
 used to characterise the protein expression from various life es of P.falciparum. Oligonucleotide primers were used to ampliicted ORF from chromosome 2 using genomic DNA as template. The
 AAACAGAAAAAAGAAAATGAAGA 369
 2000-086380/07
 23;
 SD
 SL,
 Similarity
 SEC
 gene
 Conservative
 Carucci DJ;
 B₽;
 drugs
 OF NAVY
 98US-0082947.
99US-0082947.
 99WO-US09047
 121
 entry)
 A;
 8.7%;
 58
 Ç
 0;
 Score
Pred.
 68
 Mismatches
 ç
 .
No
 146 T; 0
 DB
 6,
 22;
 other;
 0;
 form part of the
tronic format directly
 Length
 Indels
 e 2. Rifin genes
rious life cycle
d to amplify each
 2. Rifin
 0,
 gs
 Gaps
 each
 0;
```

```
RESULT
AAZ29252
밁
 Ş
 В
 Qy
 SO
 Best Loc
Matches
 Best Loc
Matches
 Query Match
 Query Match
 The present sequence is the Rifin 3194 gene of chromosome 2. Rifin genes were used to characterise the protein expression from various life cycle stages of P. falciparum. Oligonucleotide primers were used to amplify each selected ORF from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
 Rifin 3194 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid YRND50; Acccine; immunisation; stage specific protein expression; antimicrobial vaccine; antimicrobial drug; IAF; immunofluorescent antibody testing; ds
 Use
 24-APR-1998;
23-APR-1999;
 Plasmodium falciparum
 AAZ29252
 Sequence 930
 Sequence
 Claim
 Hoffman
 26-APR-1999;
 04-NOV-1999
 WO9955381-A1
 Rifin
 28-FEB-2000
 AAZ29252
 (USNA)
 877
916
 45
 45 AGAAAAAAGAAAATGAAGAAAA
 Local
 Local
 vaccine,
 IJ
 of microbial, animal and/or human genomic raccine, drug or diagnostic products -
 agaaaaaagaaaatgaagaaaa
 AGAAAAAAGAAAATGAAGAAAA
 2000-086380/07
 3194
 14; Page 16; 23pp; English.
 . Similarity
22; Conserv
 l Similarity
22; Conser
 Sn
 SL,
 969
 standard;
 SEC
 gene
 8.3%;
ilarity 100.0%;
Conservative
 Conservative
 Carucci
 BP;
 B₽;
 (first
 OF NAVY.
 98US-0082947.
99US-0082947.
 99WO-US09047.
 355
 342 A; 139
 DNA; 969
 entry)
 8.3%;
 짇
 A; 144 C;
 C;
 66
 0;
 ВP
 898
 66
 0;
937
 Score 22;
Pred. No.
 Score 22;
 Pred. No.
 178
 206
 Mismatches
 Mismatches
 <u>و</u>;
 <u>ن</u>
 264
 271 T; 0
 DB
 DB
 T; 0
 21;
 21;
 0,
 0;
 data
 other
 other;
 Length 930,
 Length 969,
 Indels
 for identification
 0;
 0;
 Gaps
 Gaps
 each
 0
 0;
```

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₹₹XB
 밁
 RESULT
 The present sequence is the Rifin 3198 gene of chromosome 2. Rifin genes were used to characterise the protein expression from various life cycle stages of p. falciparum. Oligonucleotide primers were used to amplify each selected ORF from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid vm1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
 Rifin 3198 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid VR1050; DNA vaccine; immunisation; stage specific protein expression; antinicrobial vaccine; antimicrobial drug; IAF; immunofluorescent antibody testing; ds.
 Use of microbial, animal and/or human genomic data for identification of vaccine, drug or diagnostic products -
Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalaria; malaria; protozoacide; infection; insecticide; ds.
 Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:419
 07-NOV-2000
 AAA70286;
 Sequence 978 BP; 357 A; 152 C; 208 G; 261 T; 0 other;
 Claim 16; Page 17; 23pp; English.
 WPI; 2000-086380/07.
 Hoffman SL, Carucci DJ;
 (USNA) US SEC OF NAVY.
 24-APR-1998;
23-APR-1999;
 26-APR-1999;
 04-NOV-1999
 WO9955381-A1.
 Plasmodium falciparum.
 Rifin 3198 gene.
 28-FEB-2000
 AAZ29254;
 AAZ29254 standard; DNA; 978 BP
 AAA70286 standard; DNA; 984 BP
 vaccines and drugs.
 925
 45 AGAAAAAAGAAAATGAAGAAAA 66
 6
 7
 agaaaaaagaaaatgaagaaaa 946
 Similarity
 ilarity 100.0%;
Conservative
 (first entry)
 (first entry)
 98US-0082947.
99US-0082947.
 99WO-US09047.
 8.3%;
 0;
 Score 22; DB 21; Length 978; Pred. No. 4.1;
 Mismatches
 0;
 0
 Gaps
 0
```

```
RESULT
AAA70284
ID AAA
XX
AC AAA
XX
DT 07--
XX
DE Plaa
XX
XX
XX
VX
VX
XX
AN
XX
 밁
 The present invention describes proteins and their fragments (I) encoded C by chromosome 2 of the human malarial parasite, plasmodium falciparum. CC Also described are: (I) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC antibody raised to immunogens comprising the sequences of (I), are useful in the detection with P. falciparum Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC complexity of the parasite lifecycle, and provide new targets for complexity of the parasite lifecycle, and provide new targets for cresistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC and protein sequences given in the present invention, but which are not to considerate and provide and protein sequences given in the present invention, but which are not to considerate the protein sequences given in the present invention, but which are not to considerate the protein sequences given in the present invention, but which are not to considerate the protein sequence of malarial in the present invention.
 Matches
 Query Match
Best Local :
 Plasmodium falciparum; chromosome 2; human malaria parasite; antimalarial; malaria; protozoacide; infection; insecticide;
 Plasmodium falciparum, useful as an diagnosis of P.falciparum infection
 Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
 Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:417
 07-NOV-2000
 Disclosure; Page 575; 577pp; English.
 WPI; 2000-365347/31.
 05-NOV-1998;
 05-NOV-1999;
 AAA70284;
 AAA70284 standard; DNA; 1038
 Sequence 984 BP; 360 A; 145 C; 183 G; 296 T; 0 other;
 Hoffman S, Carucci D,
 11-MAY-2000
 WO200025728-A2
 Plasmodium falciparum.
 (VENT/) VENTER J C
 (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
 Local
 æ
 1 Similarity 100.
22; Conservative
 (first entry)
 98US-0107131.
 99WO-US26796.
 8.3%; 500
100.0%; Pro
 Gardner M, Venter JC;
 Score 22;
Pred. No.
 Mismatches
 DB 21; Length 984;
 0;
 Indels
 0;
 Gaps
 0
```

```
RESULT
AAA7029
ID AAA77
XX AAA7
AC AAA7
XX AAA7
XX Plas
XX Plas
XX Plas
XX Plas
XX Plas
XX Plas
 Q
 밁
 The present invention describes proteins and their fragments (I) encoded CD by chromosome 2 of the human malarial parasite, Plasmodium falciparum. CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC P. falciparum infection. (I) and polyclonal antisera or a monoclonal CC antibody raised to immunogens comprising the sequences of (I), are CC useful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC infection, or they can be used to identify drug resistance in CC us sequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite lifecycle, and provide new targets for CC vaccine and drug development. Parasite resistance to drugs and mosquito CC parts of the world, and there is a pressing need for vaccines and new CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not CC creci fically mentioned within the specifically mentioned for Matches
 Query Match
Best Local
 (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
 Proteins encoded by chromosome 2 of the human plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
 Disclosure;
 WPI; 2000-365347/31
 05-NOV-1998;
 05-NOV-1999;
 11-MAY-2000.
 Plasmodium falciparum
 antimalarial; malaria;
 07-NOV-2000
 AAA70279 standard; DNA; 1047
 Sequence 1038 BP; 379 A; 157 C; 209 G;
 specifically mentioned within the specification.
 Hoffman
 Plasmodium falciparum
 Plasmodium falciparum;
 Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:412
 AAA70279;
 985
 45 AGAAAAAAGAAAATGAAGAAAA 66
 Local
 ø
 agaaaaaagaaaatgaagaaaa 1006
 22;
 ş
 Similarity
 Carucci
 Conservative
 Page 574-575;
 (first entry)
 99WO-US26796
 98US-0107131
 Á
 100.0%;
 8.3%;
 chromosome 2; human malaria parasite;
protozoacide; infection; insecticide;
 Gardner M,
 577pp;
 0,
 Score 22;
Pred. No.
 ВP
 Mismatches
 English.
 Venter JC;
 293 т;
 DB 21;
 malarial vaccines
 0 other;
 0
 Length 1038;
 Indels
 parasite,
and in the
 0;
 vaccine;
 Gaps
 0,
```

```
ABL18816
 В
 Ş
 RESULT 10
 CC (I) and (II) are useful for the development of vaccines against
CC (P) falciparum infection. (I) and polyclonal antisera or a monoclonal
CC antibody raised to immunogens comprising the sequences of (I), are
CC antibody raised to immunogens comprising the sequences of (I), are
CC (I) (especially when they are rifins or secreted or membrane proteins)
CC can aid the identification of drugs to treat or prevent P. falciparum
CC infection, or they can be used to identify drug resistance in
CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
CC subsequent identification of proteins encoded by it will help to expand
CC our understanding of parasite biology, a process hampered by the
CC complexity of the parasitic lifecycle, and provide new targets for
CC vaccine and drug development. Parasite resistance to drugs and mosquito
CC resistance to insecticides have led to a resurgence of malaria in many
CC parts of the world, and there is a pressing need for vaccines and new
CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
CC specifically mentioned within the specification.
 Best Local
Matches :
 Query Match
 (HOFF/)
(CARU/)
(GARD/)
 Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection -
 pharmaceutical;
 Drosophila
 Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).
 Disclosure;
 WPI; 2000-365347/31
 05-NOV-1998;
 11-MAY-2000
 Drosophila;
 26-MAR-2002
 ABL18816;
 ABL18816 standard; DNA; 29783
 Sequence
 The present invention
 Hoffman S,
 (VENT/)
 05-NOV-1999;
 WO200025728-A2
 994 agaaaaaagaaaatgaagaaaa 1015
 45 AGAAAAAAGAAAATGAAGAAAA 66
 chromosome
 HOFFMAN S.
CARUCCI D.
GARDNER M.
 . Similarity 100 22; Conservative
 VENTER J C
 1047
 melanogaster genomic polynucleotide SEQ ID NO 7921
 developmental biology; cell signalling; insecticide;
cal; gene; ds.
 Page 573;
 Carucci
 (first entry)
 B₽;
 98US-0107131
 99WO-US26796
 ention describes proteins and their fragments (I) encoded of the human malarial parasite, Plasmodium falciparum.
 383
 Ď
 8.3%;
 A; 163 C;
 577pp;
 Gardner M,
 0;
 Score 22;
Pred. No
 English.
 ВP
 211 G;
 Mismatches
 No.
 Venter JC;
 290 T;
 DΒ
 21;
 0 other;
 0;
 Length 1047;
 Indels
 parasite, and in the
 0;
 the
 Gaps
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0;

Drosophila melanogaster

WO200171042-A2

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RESULT 11
AAI81813/c
ID AAI818
 밁
 ACC XXX ACC XX
 Š
 Query Match
Best Local Similarity
Matches 22; Conserv
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 Claim 1; SEQ ID NO 7921; 21pp + Sequence Listing; English.
 New isolated nucleic acid genes from Drosophila and interactions -
 Venter
 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
 23-MAR-2001; 2001WO-US09231.
 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
 06-NOV-2001 (first entry)
 AAI81813 standard; cDNA; 471
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 (PEKE) PE CORP
 28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
 07-SEP-2001
 Homo sapiens.
 Human polynucleotide SEQ ID NO 1873.
 Sequence 29783 BP; 7503 A; 6790 C; 6798 G; 8692 T; 0 other;
 (HYSE-) HYSEQ INC
 26-FEB-2001; 2001WO-US04927.
 WO200164835-A2
 2001-656860/75.
 JC, Adams M,
 8.3%; ilarity 100.0%; Conservative
 Li PWD,
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
 0;
 Score 22;
Pred. No.
 BP
 Myers EW;
 Mismatches
 DB 23; Length 29783; 3.8;
 0;
 Indels
 0;
 Gaps
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 0
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В
 δÃ
 Query Match
Best Local Similarity
Matches 21; Conserv
 04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-UUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEB-2000; 2000US-0234687.

27-SEB-2000; 2000US-023659.

04-OCT-2000; 2000GB-0024263.
 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
 WPI; 20
P-PSDB;
 Tang
 Probe; microarray; human; placenta; antenatal diagnosis,
genetic disorder; ss.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Claim 1; SEQ ID NO 1873; 1399pp + Sequence Listing; English
 Sequence
 WPI; 2001-488897/53
 09-AUG-2001
 WO200157272-A2
 Probe #13075 used to measure gene expression in human placenta
 17-OCT-2001 (first entry)
 AAI44389 standard; DNA; 588 BP
 Penn SG,
 30-JAN-2001; 2001WO-US00663.
 Homo sapiens.
 (MOLE-)
 2001-514838/56.
DB; AAO01882.
 MOLECULAR DYNAMICS INC
 471 BP; 121 A; 123 C; 126 G; 97 T; 4 other;
 Liu C,
 Hanzel DK,
 7.9%; So llarity 100.0%; I Conservative 0;
 Drmanac
 Chen W,
 Score 21; DB 22; Length 471; Pred. No. 11; 0; Mismatches 0; Indels
 Rank DR;
 and immune
 0;
 Gaps
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SXXCCCCCXXX PT

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RRSSULT 1
ID AAZ2925
XX AZ2925
XX AZ2
 Matches
 Query Match
Best Local Similarity
 Human geno
analyzing
 The
 The present sequence is the Rifin 3201 gene of chromosome 2. Rifin genes were used to characterise the protein expression from various life cycle stages of P.falciparum. Oligonucleotide primers were used to amplify each selected ORR from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to desire the control of the cont
 Use
 WPI;
 The
 Claim 18;
 of vaccine,
 24-APR-1998;
23-APR-1999;
 04-NOV-1999
 WO9955381-A1
 Plasmodium falciparum.
 antimicrobial
 mammalian expression plasmid VR1050; DNA vaccine; immunis stage specific protein expression; antimicrobial vaccine;
 producing a microarray
 Claim
 Hof fman
 26-APR-1999;
 Rifin 3201 gene;
 Rifin 3201
 28-FEB-2000
 AAZ29256;
 AAZ29256 standard;
 Sequence 588
 expression in
 identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial vaccines and drugs.
 (USNA)
 218
 172 TAAGAAAGAATTAAAAGAAAA
 Local
 13
 present invention relates to single exon nucleic acid probes present sequence is one such probe. The probes are useful for ducing a microarray for predicting, measuring and displaying gression in samples derived from human placenta. The probes are antenatal diagnosis of human genetic disorders.
 of microbial, animal and/or human
 taagaaagaattaaaagaaaa
 2000-086380/07
 genome-derived single exon nucleic acid probes useful zing gene expression in human placenta -
 SL,
 SD
 SEQ ID No 13075; 654pp; English.
 Page 17; 23pp; English
 SEC
 gene
 drug
 Conservative
 BP;
 Carucci
 (first
 drug; IAF; immunofluorescent
 OF NAVY
 98US-0082947.
99US-0082947.
 99WO-US09047.
 or diagnostic products
 P.falciparum chromosome 2; Rifin
 280 A; 84
 DNA;
 entry)
 Ď.
 100.0%;
 7.98;
 936
 238
 192
 c;
 ВP
 0;
 Score 21;
Pred. No.
 115
 Mismatches
 G;
 109
 genomic data for identification
 DB
 T; 0 other;
 antibody testing; ds
 22;
 0,
 Length
 protein;
immunisation;
 Indels
 588;
 probes are useful
 for
 0,
 Gaps
 gene
 (SENP).
 each
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Sequence

936

B₽;

357

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136

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190

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253

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Query Match Best Local S Matches 21

. Similarity 21; Conserv

Conservative

0

Mismatches

0;

Indels

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Gaps

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No.

11;

22;

Length 976;

7.98;

Score 21; Pred. No

Sequence

BP;

Α,

Ç

other

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RESULT
AAH33151
 Вb
 Qy
 Query Match
Best Local
 Matches
 cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of coloractial carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
 present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
 AAH33151;
 AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human
 29-SEP-1999;
03-NOV-1999;
 Human
 03-SEP-2001
 AAH33151 standard;
 Claim 1;
 usetul
 Nucleic
 (HUMA-) HUMAN GENOME
 28-SEP-2000;
 05-APR-2001
 WO200122920-A2
 Homo
 colorectal carcinoma;
 884 gaaaaaagaaaatgaagaaaa
 46 GAAAAAAGAAATGAAGAAAA
 sapiens.
 2001-235357/24
 MS,
 colon
 c acids encoding 4277 human colon cancer-associated polypeptides,
for preventing, diagnosing and/or treating colorectal cancers -
 colon
 Similarity
 976
 Page 2352; 9803pp; English.
 cancer antigen
 cancer; colon cancer antigen; diagnosis; detection;
arcinoma; chromosome 16; ss.
 Conservative
 (first entry)
 2000WO-US26524
 99US-0157137.
99US-0163280.
 431
 SC
 cDNA;
 SCI INC
 100.0%;
 7.9%;
 Birse
 164
 976
 encoding cDNA SEQ ID NO:207
 904
 66
 0,
 Score 21;
Pred. No.
 Œ,
 ВP
204 G;
 Mismatches
 Rosen
 168
 DB
11;
 CA
 Η,
 sequence listing were sequences are present
 21;
 0
 Length 936;
 Indels
 present
 0;
 colon
 Gaps
 for
 0;
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RESULT 15
AAA70079
ID AAA700
 밁
 The present invention describes proteins and their fragments (I) encoded CD by chromosome 2 of the human malarial parasite, plasmodium falciparum. CC Also described are: (I) nucleotide sequences (II) encoding (I): and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against P. falciparum infection of and polyclonal antisers or a monoclonal CC antibody raised to immunogens comprising the sequences of (I), are CC useful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC infection, or they can be used to identify drug resistance in CC subsequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC subsequent identification for the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC parts and drug development. Parasite resistance to drugs and mosquito CC resistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide CC and protein sequences given in the present invention, but which are not xx
 Ouery Match 7.9%; Score 21; DB 21; Length 1005; Best Local Similarity 100.0%; Pred. No. 11; Matches 21; Conservative 0; Mismatches 0; Indels
 (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
 Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
 05-NOV-1998;
 05-NOV-1999;
 11-MAY-2000.
 Plasmodium falciparum.
 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide; ds.
 Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:212
 07-NOV-2000 (first entry)
 AAA70079;
 AAA70079 standard; DNA; 1005 BP
 WO200025728-A2.
 Disclosure; Page 448-449; 577pp; English.
 WPI; 2000-365347/31.
 Hoffman S, Carucci D,
 Sequence 1005 BP; 381 A; 145 C; 196 G;
 98US-0107131.
 99WO-US26796.
 Gardner M, Venter JC;
 283 T;
 0 other;
 0;
Gaps
 0
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Дb
 QY
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Search completed: August 3, 2002, 01:52:42 Job time: 32347 sec

| 3 2 4 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . 24 4 . | Scc                             | and is               | Pred. No.                                                                                                                                                                                                          |                                                                                                                                            | Database :          | Post-processing:           | Minimum DB seq l<br>Maximum DB seq l | Total number of                    | Word size :                                       | Searched:                          | Scoring table:                                 | Title: Perfect score: Sequence:                                                   | Run on:                                                                                 | OM nucleic - nuc                                     |                                                           |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------|----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|---------------------|----------------------------|--------------------------------------|------------------------------------|---------------------------------------------------|------------------------------------|------------------------------------------------|-----------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|------------------------------------------------------|-----------------------------------------------------------|
| 9.1 343 9 AA74553<br>9.1 375 12 AZZJ3624<br>9.1 430 9 AL69918<br>9.1 456 9 AA69918<br>9.1 485 12 AQS00417<br>9.1 539 12 AQS00417<br>9.1 657 12 AQS22151<br>9.1 677 10 BM015597<br>9.1 877 10 BEZ39967<br>9.1 87372 9 AUGS3257<br>8.7 372 9 AUGS3257<br>8.7 393 9 AA658426<br>8.7 683 9 AL653095<br>8.7 683 9 AL653095<br>8.7 743 12 AG032665                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ry<br>ch Length DB<br>.2 882 12 | by analysis of the t | ,                                                                                                                                                                                                                  | 2: em_esthum:* 4: em_estin:* 5: em_estov:* 5: em_estov:* 7: em_estov:* 9: em_estov:* 10: gb_est1:* 11: gb_est2:* 11: gb_est2:* 12: ch_gs:* | EST:* 1: em_estba:* | Listing first 45 summaries | length: 0<br>length: 2000000000      | hits satisfying chosen parameters: | 0                                                 | 13736207 segs, 6748477542 residues | OLIGO_NUC<br>Gapop 60.0 , Gapext 60.0          | US-08-973-363-12 265 1 GATGAGATTGTTTCAGTGAAAAG                                    | 22:41:57 ; s                                                                            | nucleic search, using sw model                       | GenCore version 4.5<br>Copyright (c) 1993 - 2000 Compugen |
| AA748563 035709.s AA748563 035709.s AA7213624 Sheared D AI742163 qh81f02.x AA699918 z161f12.s AA699918 z16112.s AA69918 z16939170 AA759846 AA699170 AA759846 nu18e11.s AA658426 nu18e11.s AL633205 AL633205 BI640191 SD23001.5 AG032665 Pan trog1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Description AZ184391 SP_1002_B  | score distribution.  | predicted by chance to have a                                                                                                                                                                                      |                                                                                                                                            |                     |                            |                                      | 27472414                           |                                                   |                                    |                                                | AAGAAGTGAAGGAAGAGAAG 265                                                          | Search time 7016.61 Seconds<br>(without alignments)<br>509.747 Million cell updates/sec |                                                      | n Utd.                                                    |
| FEATURES<br>SOU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | JOURNAL<br>MEDLINE<br>COMMENT   | TITLE                | SOURCE<br>SOURCE<br>ORGANISM<br>REFERENCE                                                                                                                                                                          | RESULT 1 AZ184391 LOCUS DEFINITION ACCESSION VERSION KEYWORDS                                                                              |                     | C 44<br>45                 |                                      | 000                                |                                                   | 0 (                                |                                                | იი                                                                                | n                                                                                       | O                                                    | იი                                                        |
| ä                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | INE                             | E 020                | NISM DS                                                                                                                                                                                                            | TION                                                                                                                                       |                     |                            |                                      | -04                                | 000 \                                             | 36                                 | , ww.                                          | 30<br>31<br>31                                                                    | 25<br>27<br>28                                                                          | 222                                                  | 18<br>19<br>20                                            |
| rce .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | AL.                             |                      | ,34                                                                                                                                                                                                                | N ON 1                                                                                                                                     |                     |                            |                                      | 121                                | 22                                                | 22                                 | 222                                            | , , , , , ,<br>, , , , , ,                                                        | 22222                                                                                   | 222                                                  | 2888                                                      |
| California Pasadena Pal: (526 Fax: (626 Email: ac Email: ac Plate: 10 Seq prime Class: Bh High qual                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AL.                             |                      | strongyl strongyl strongyl Eukaryot Echinoid Strongyl strongyl to base                                                                                                                                             | N ON 1                                                                                                                                     |                     | 7.9 355                    | 7.9 254                              | 21 7.9 165                         | 22 8.3 1248<br>22 8.3 1248                        | 22 8.3 980                         | 22 8.3 884<br>22 8.3 938<br>33 938             | 22 8.3 584<br>22 8.3 616<br>22 8.3 619<br>22 8.3 876                              | 22 8.3 518<br>22 8.3 520<br>22 8.3 554<br>22 8.3 560                                    | 22 6.3 104<br>22 8.3 301<br>22 8.3 413<br>22 8.3 415 | 23 8.7 826<br>23 8.7 867<br>23 8.7 920                    |
| California I Pasadena Cal Pasadena (626) 3 Pel: (626) 3 Pal: (626) 7 Email: acame Plate: 1002 Seq primer: Class: BAC e High quality I Crce 1. /cl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | AL.                             |                      | SSS: Strongylocentrotus purpuratus. Strongylocentrotus purpuratus Strongylocentrotus purpuratus Eukaryota; Metazoa; Echinodermata; El Echinoidea; Eucchinoidea; Echinacea; Strongylocentrotidae; Strongylocentroti | 1 AZ184391 AZ184391 ON SP_1002_B2_G05_T7A Stron . sperm genomic BAC libr . clone Plate-1002 Col-10 AZ184391 AZ184391.1 GI:8356766          | ALIGNMENTS          | 7.9                        | 7.9 254 9                            | 21 7.9 165 9 2                     | 22 8.3 1062 12<br>22 8.3 1248 10<br>21 7.9 148 10 | 22 8.3 980                         | 22 8.3 884 9<br>22 8.3 938 12<br>22 8.3 938 12 | 22 8.3 584 10<br>22 8.3 616 12<br>22 8.3 619 12<br>22 8.3 619 12<br>22 8.3 876 12 | 22 8.3 518 12<br>22 8.3 518 12<br>22 8.3 520 10<br>22 8.3 554 10<br>22 8.3 560 10       | 22 6.3 104<br>22 8.3 301<br>22 8.3 413<br>22 8.3 415 | 23 8.7 826 12<br>23 8.7 867 12<br>23 8.7 920 12           |

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BASE COUNT
ORIGIN
 SOURCE
 BASE COUNT
ORIGIN
 B
 QΥ
 FEATURES
 COMMENT
 REFERENCE
 KEYWORDS
 VERSION
 DEFINITION
 ACCESSION
 LOCUS
 AZ091555
 RESULT
 Query Match
Best Local
 AUTHORS
 ORGANISM
Query Match
Best Local Similarity
 source
 145 GAAAAGGGAGAAAAAAGAAAAAGAGGA 171
 532 GAAAAGGGAGAAAAAAGAAAAAGAGGA 558
 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 27 row: F column: 16
 Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researc
 Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-27F16.TJ
 GSS
 RPCI-23-27F16.TV RPCI-23
 Class: BAC ends.
 Zhao,S., Nierman,W., Feldblyum,T.,
,B., Levins,M., Mcgann,S., Tsegaye
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Mus musculus
 DNA sequence.
 AZ091555.1 GI:7733598
 nouse mouse
 Similarity
 (bases
 Medical Center Dr., Rockville, 301 838 0200 301 838 0208 1: 0.00
 primer: T7
 377
 226
 Conservative
 ۵ı
 /note-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " a 130 c 94 g 140 t
 urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
 DH10B"
 /clone_lib="RPCI-23"
 /db_xref="taxon:10090"
/clone="RPCI-23-27F16"
 /organism="Mus musculus"
/strain="C57BL/6J"
 Location/Qualifiers
 1 to 590)
 /lab_host="DH10B"
 /sex="Female"
 10.2%;
9.8%;
100.0%;
 51 c
 Chordata;
Rodentia;
 0;
 Score 27;
Pred. No.
 Score
Pred.
 304 g
 590 bp DNA linear GSS 08-MAY-2000 Mus musculus genomic clone RPCI-23-27F16,
 Mismatches
 lyum,T., Malek,J., Sha
Tsegaye,G., Geer,K.,
 26;
No.
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 67 t
 DB 12;
9.2;
 DB 12;
 .7;
 MD 20850, USA
 0;
 Length 882;
 83 others
 Length 590;
 Shatsman, S.,
 0;
 Gaps
 Akinret
 0,
```

```
REFERENCE
AUTHORS
 RESULT 3
AA748563/c
 VERSION
KEYWORDS
 В
밁
 20
 FEATURES
 COMMENT
 Qy
 ORIGIN
 BASE COUNT
 SOURCE
 ACCESSION
 DEFINITION
 LOCUS
 Matches
 Matches
 JOURNAL
 TITLE
 ORGANISM
 source
 375
 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 32
 Local
AAAAGAAAAAGAGGATAAGAAAGA 29
 AAAAAATAAAAACAGAAAAAAAAAAAA 400
 AAAAATAAAACAGAAAAAAGAAAA
 AA748563

AA748563

AA748563

AA7609.S1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1309072 3' similar to SW:CHD1_MOUSE P40201 CHROMODMAIN-HELICASE-DNA-BINDING PROTEIN CHD-1. [1] ;contains element L1 repetitive element ;, mRNA
 th 9.1%; Score 24;

l Similarity 100.0%; Pred. No.

24; Conservative 0; Mismatc
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1312 Std Error: 0.00
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D.,
 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Homo sapiens
 AA748563
 26;
 High quality sequence stop: 282.
Location/Qualifiers
 Bonaldo, Ph.D.
 Unpublished (1997)
 AA748563.1 GI:2788521
 Seq primer:
 Eukaryota; Metazoa;
 (bases 1 to 343)
 Conservative
 62
 Gene Index
 þ
 j. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

3 5 g 177 t
 /clone="IMAGE:1309072"
/clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
/lab_host="DH10B"
 /organism="Homo sapiens"
/db_xref="taxon:9606"
 Eutheria;
 -40ml3 fwd. ET from Amersham
 Chordata;
Primates;
 0;
 57
 Mismatches
 Mismatches
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 DB 9;
54;
 0,
 Length 343;
 Indels
 Indels
 Ph.D.,
 Sequencing Center
information can be
 David Allman,
 .
 0,
 0;
 Fatima
 Gaps
 Gaps
 0
 0;
```

```
RESULT 5
AI242163/c
 ACCESSION
VERSION
KEYWORDS
 RESULT 4
AZ213624/c
 밁
 ORIGIN
 FEATURES
 COMMENT
 VERSION
 ACCESSION
 DEFINITION
 BASE COUNT
 REFERENCE
 SOURCE
 DEFINITION
 Matches
 Query Match
Best Local
 TITLE
 AUTHORS
 ORGANISM
 source
 172 TAAGAAAGAATTAAAAGAAAAAGA 195
 308 TAAGAAAGAATTAAAAGAAAAAGA 285
 9712 Medical
Tel: 301 838
Fax: 301 838
 Contact: Najib M. El-Sayed
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
 AZ213624 375 bp DNA linear GSS 09-JUN-2000 Sheared DNA-113F9.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-113F9, DNA sequence.
AI242163
AI242163.1 GI:3837560
 A1242163 430 bp mRNA linear EST 01-DEC-1998 qh816102 x1 Soares_fetal_liver_spleen_LNFLS_S1 Homo sapiens cDNA clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
 Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through Research Genetics, Alabama, USA. Sheared DNA
end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
 El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
 element ; , mRNA sequence.
 Class: shotgur
 Trypanosoma brucei.
 GSS
 AZ213624.1 GI:8431424
 Similarity
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 (bases 1 to 375)
 primer: M13-Forward
 301 838 0200
301 838 0208
 94 a
 Conservative
 _GSSs: Sheared DNA-113F9.TR
 Press, 1.
 /note-"vector: DUCIB: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREB927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University press, 1999)."
 /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
 /clone="Sheared DNA-113F9"
/clone_lib="Sheared DNA"
 /db_xref="taxon:5691"
 Location/Qualifiers
 9.1%; 50-
100.0%; Pro
 Score 24; DB 12; Length 375; Pred. No. 53;
 70 g
 Mismatches
 430 bp
 143 t
 0,
 0;
 0
```

```
RESULT 6
AA699918/c
 SOURCE
ORGANISM
 COMMENT
 밁
 ORIGIN
 BASE COUNT
 FEATURES
 COMMENT
 REFERENCE
 SOURCE
 ACCESSION
 DEFINITION
 REFERENCE
 KEYWORDS
 KEYWORDS
 TITLE
 ORGANISM
 Matches
 Query Match
Best Local :
 TITLE
 AUTHORS
 JOURNAL
 AUTHORS
 source
 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 51 AAAAGAAAAAGAGGATAAGAAAGA 28
 Local Similarity
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 456)

RS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RX

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 AA699918 456 bp mRNA linear EST 19-DEC: zi61F12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435311 3 , mRNA sequence.
 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1274 Std Error: 0.00
 EST
 Homo sapiens
 High quality sequence stop: 429.
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
 Homo sapiens
 human.
 AA699918.1 GI:2702881
 111 a
 Conservative
 liver spleen lNFLS library. Ist strand cDNA was primed with a Pac I - oligo(dT) primer [5' ALTGGAAGAATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pag I; Site_2: Eco R; This is a subtracted version of the original Soares fetal liver spleen lNFLS library. 1st strand cDNA was primed
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/clone="IMAGE:1851099"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
 /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
 Location/Qualifiers
 /organism="Homo sapiens"
 -40UP from Gibco
 9.1%; Score 24; DB 9; Length 430; 100.0%; Pred. No. 51;
 0; Mismatches
 Indels
 EST 19-DEC-1997
 0,
 Gaps
```

```
KEYWORDS
SOURCE
ORGANISM
 RESULT
AQ642393
 REFERENCE
 BASE COUNT
ORIGIN
 FEATURES
FEATURES
 VERSION
 ACCESSION
 DEFINITION
 TITLE
 Matches
 Query Match
Best Local
 AUTHORS
 source
 157 AAAAGAAAAAGAGGATAAGAAAGA 180
 47
 AAAAGAAAAGAGGATAAGAAAGA 24
 Library for gene discovery and sequence-ready map construction unpublished (1999)
Other_GSSs: RPC193-DpnII-28K15.TJ
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
 El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
 AQ642393 AQ642393 AQ642393 DNA linear GSS 08-JUL-1999 RPCI93-DpnII-28K15.TV RPCI93-DpnII Trypanosoma brucei genomic clone RPCI93-DpnII-28K15, DNA sequence.
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham
 Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences
 Trypanosoma brucei
 High quality sequence stop: 420.
Location/Qualifiers
 Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma brucei.
 AQ642393.1 GI:5119103
 Class: BAC ends.
 Similarity
 e: http://www.tigr.org/tdb/mdb/tbdb/.
primer: T7
 bases 1 to 485)
 119
 Conservative
 est@watson.wustl.edu
 /lab_host-"DH10B (ampicillin resistant)"
/note-"Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Sit__1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lnFLS library. 1st strand cDNA was primed
 constructed by Bento Soares and M.Fatima Bonaldo."
95 c 57 g 185 t
Location/Qualifiers
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/clone="IMAGE:435311"
 /organism="Homo sapiens"
/db_xref="GDB:1335080"
 /dev_stage="20 week-post conception fetus"
 /sex="male"
 /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
 9.1%;
 0; Mismatches
 Score 24;
Pred. No.
 50;
 9
 0;
 Length 456;
 Indels
 0;
 Gaps
 the Pac
 search
 0;
```

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VERSION
KEYWORDS
 RESULT 8
AQ500417/c
LOCUS
 FEATURES
 COMMENT
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 Qy
 REFERENCE
 DEFINITION
 ORIGIN
 BASE COUNT
 ACCESSION
 Query Match
Best Local S
Matches 24
 TITLE
 AUTHORS
 ORGANISM
 JOURNAL
 source
 172 TAAGAAAGAATTAAAAGAAAAAGA 195
 64
 TAAGAAAGAATTAAAAGAAAAAAA 87
 P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
 Contact: Kumar A
Michael Snyder, Dept.
 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
 baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 AQ500417.1 GI:4706127 GSS.
 AQ500417 539 bp DNA linear G
V40B12 mTn-3xHA/lacZ Insertion Library Saccharomyces
genomic 5', DNA sequence.
AQ500417
 Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
 Unpublished (1999)
 Gene Disruption
 Yale University
 Similarity
 (bases 1 to 539)
 172
 primer: GGCCTTCTTTCTTTGGAAGTAC
ss: transposon-tagged.
 9.1%; Score 24; DB ilarity 100.0%; Pred. No. 50 Conservative 0; Mismatches
 /organism="Trypanosoma brucei"
/strain="TrRED927/4 GUTat 10.1"
/db_xref="Taxon:5691"
/clone="RPCI93-DpnII-28K15"
/clone="RPCI93-DpnII"
/clone="Vector: pBACe3.6; Site_1: Bam HI; Site_2: Bam HI;
Constructed for The Institute for Genomic Research by
Bohui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucei TRED927/4 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPCI93-EcoRI segment) or Dpn II (RPCI93-DpnII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam H1,
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 X the haploid
non-minichromosomal genome."
172 a 91 c 68 g 153 t 1 others
 þ
 /lab_host="E. coli"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
(lacking mitochondrial DNA) was prepared in pHSS6-Sal;
genomic DNA was size-fractionated (DNA of roughly 2-3 kb
in length) prior to cloning. This library was
subsequently mutagenized with a mTn-3xHA/lacz
 /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/clone_lib="mTn-3xHA/lacZ Insertion Library"
 Location/Qualifiers
 of Mol.
 Cell. and
 DB
50;
 12;
 0;
 Dev. Biology
 Length 485
 GSS 29-APR-1999
 cerevisiae
 0;
resistance."
 Gaps
 0,
```

Page 5

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COMMENT
 밁
 ORIGIN
 BASE COUNT
 FEATURES
 REFERENCE
 DEFINITION
 BASE COUNT
 VERSION
 ACCESSION
 AQ952151/c
 EYWORDS
 Query Match
 TITLE
 AUTHORS
 ORGANISM
 Matches
 source
 145 GAAAAGGGAGAAAAAAGAAAAAAA 168
 257 GAAAAGGGAGAAAAAAGAAAAAAA 234
 Local Similarity
 Local Similarity
 Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 AQ952151 643 bp DNA linear GSS 27-JAN-21 Sheared DNA-42C8.TF Sheared DNA Trypanosoma brucei genomic clone
 Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
 Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
 El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat
 Sheared DNA-42C8, DNA sequence.
 AQ952151
 Other_GSSs: Sheared DNA-42C8.TR
 Unpublished (1999)
 Trypanosoma brucei.
 Seq primer: M13-Forward
 AQ952151.1 GI:6775416
 10.1 sheared DNA library
 188 a
 (bases 1 to 643)
 Medical Center Dr., Rockville, MD 20850, USA 301 838 0200 301 838 0208
 Conservative
 58 a
 /organism="Trypanosoma brucei"
/ostrain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/db_xref="taxon:5691"
/clone="Sheared DNA-42C8"
/clone="Sheared DNA-42C8"
/clone="Sheared DNA-42C8"
/clone="Vector: puC18: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert librarles for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Process 1000 v."
 Location/Qualifiers
9.1%; Score 24; DB 12; Length 643; 100.0%; Pred. No. 46;
 135 c
 142 c
 100.0%;
 , 1999).
111 g

 Mismatches

 Score 24;
Pred. No.
 24 g
 208 t
 315 t
 DB 12;
48;
 0; Indels
 Length 539;
 1 others
 GSS 27-JAN-2000
 0; Gaps
 0;
 g
 BASE COUNT
ORIGIN
 LOCUS
```

Ş

172 TAAGAAAGAATTAAAAGAAAAAGA 195

Matches

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

Query Match

Best Local Similarity

Matches

Conservative

0,:

Mismatches

0;

0;

Gaps

0;

9.1%; Score 24; DB 12; Length 657; 100.0%; Pred. No. 46;

```
SOURCE
ORGANISM
 FEATURES
 COMMENT
 REFERENCE
 KEYWORDS
 VERSION
 ACCESSION
 DEFINITION
 AZ508184/c
 RESULT 10
 TITLE
 AUTHORS
 source
 172 TAAGAAAGAATTAAAAGAAAAAGA 149
 High quality sequence stop: 657
Location/Qualifiers
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longare,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 AZ508184 657 bp DNA linear GSS 05-OCT-200 1M0350G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0350G18 F, DNA sequence.
 Tel: 801 585 5606 Fax: 801 585 7177
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 657)
 AZ508184
 Seq primer: CGTTGTAAAACGACGGCCAGT
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0350 row: G column: 18
 Unpublished (2000)
 plasmid inserts
 Mouse whole genome scaffolding with paired end reads from 10kb
 Mus musculus
 house mouse.
 AZ508184.1 GI:10689500
 lass: plasmid ends
 308,
 182 a
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4733114/gblAF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for amplicillin resistance."
 USA
 musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
 /note="Vector:
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /strain="C57BL/6J"
/db_xref="taxon:10090"
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /sex="Male"
 /clone="UUGC1M0350G18"
 /organism="Mus musculus"
 Std Error: 0.00
 PWD42nv; Purified genomic DNA
 GSS 05-OCT-2000
 from M.
```

29

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RESULT :
 밁
 Š
 BASE COUNT
ORIGIN
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 BF239967
 RESULT
 FEATURES
 COMMENT
 SOURCE
 REFERENCE
 SOURCE
 KEYWORDS
 DEFINITION
 REFERENCE
 KEYWORDS
 VERSION
 ACCESSION
 DEFINITION
 VERSION
 ACCESSION
 Query Match
Best Local S
Matches 24
 AUTHORS
TITLE
 AUTHORS
TITLE
 ORGANISM
 ORGANISM
 JOURNAL
 source
 298
 ATAAAAAATAAAAACAGAAAAAA 52
 mRNA sequence
BF239967
 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129
 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12066 row: g column: 08
High quality sequence stop: 674.
Location/Qualifiers
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
 BM015597
603641828F1 NIH_MGC_87
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Homo sapiens
 EST
 BF239967.1 GI:11153890
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Homo sapiens
 EST
 mRNA sequence.
 Contact: Robert Strausberg, Ph.D
 Unpublished (1999)
 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 BM015597.1 GI:16529951
 National Institutes
 NIH-MGC http://mgc.nci.nih.gov/.
 numan
 Similarity
 CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 (bases 1 to 821)
 (bases 1 to 677)
 305
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
05 a 92 c 153 g 127 t
 9.1%; Score 24;
100.0%; Pred. No.
tive 0; Mismatc
 Chordata;
Primates;
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Primates;
of Health, Mammalian Gene Collection (MGC)
 Pred. No. 46
; Mismatches
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 Homo sapiens cDNA clone IMAGE:5417887 5',
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 EST 30-OCT-2001
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 Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
 DNA Res. 5 (6), 335-340 (1998)
99156227
 Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
 Dictyostelium discoideum Eukaryota; Mycetozoa; Dictyostelium 1 (bases 1 to 372)
 discoideum
AU039357
 AU039357 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L/CM1033 row: k column: 18
High quality sequence_stop: 562.
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 PROJECT =
 Email: d402hu@sakura.cc.tsukuba.ac.jp
 Contact: Hideko Urushihara
 development
 Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
 Dictyostelium discoideum.
 AU039357.1 GI:4008597
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
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 345
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Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTRACGGCCGACATG-dT[30]BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
45 a 149 c 190 g 137 t
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 ch 8.7%; Score 23; DB 9; L
1 Similarity 100.0%; Pred. No. 1.2e+02;
23; Conservative 0; Mismatches 0;
 Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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1 (bases 1 to 393)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
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 Contact: Robert Strausberg, Ph.D.
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Matches 23
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517 AAATAAAAACAGAAAAAAAGAAAA 539
 35 AAATAAAAACAGAAAAAAAGAAAA 57
 41 AAACAGAAAAAAGAAAATGAAGA 63
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 xenopodinae; Silurana.

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Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
 EST.
western clawed frog.
western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
 mRNA sequence.-
AL653205
 23;
 Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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 AL653205 XGC-gastrula Silurana tropicalis cDNA clone
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TROPICALIS_SEQUENCE_ID: TGas049n16.sp6
 Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST
 Sanger Centre
 AL653205.1 GI:17664069
 Hinxton, Cambridgeshire, CB10 1SA,
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 Conservative
 8.7%;
llarity 100.0%;
Conservative
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into pCS107 with EcoRI at the 5' end and NotI at the 3'
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Search time (sec): 4908.870000
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gb_htg:AC099734
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AVIAN GHD GENES AND THEIR USE IN METHODS
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Gene 197 (1-2), 225-229 (1997)
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 Other publication AU 5906996 961224.
Location/Qualifiers
 Glasgow
 Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University
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 HTG 27-JAN-2002
 Murinae; Mus
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REFERENCE

AUTHORS JOURNAL REFERENCE

AUTHORS TITLE

KEYWORDS VERSION

JOURNAL

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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Plerre,M., Pollara,V., Raymond,C., Retta,R., Riaback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schuer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N. Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., WuX., Wyman,D., Ye,W.J., Young,G., Zandoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Submitted (27-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
 Direct Submission
 NOTE: This record contains 77 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
 will be sequenced to completion. In the event that
 Center code: WIBR
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14595 15328: con
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 7239 7338:
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5 7238: contig of 7
 3007: contig of (
18 5707: gap of 100
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100 bp
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contig of 728 b
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100 bp i

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 EU Arabidopsis sequencing, project.

Direct Submission
Submitted (20-SEP-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Bevan, M., Terryn, N., Ardiles, W., Buysshaert, C., Dasseville, R. Clerck, R., De Keyser, A., Neyt, P., Rouze, P., Van Den Daele, H., Villaroel, R., Gielen, J., Van Montagu, M., Bancroft, I., Mewes, H. Mayer, K.F.X., Lemcke, K. and Schueller, C.
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 Unpublished
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HTG 20-DEC-2001

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Hale, S.,

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intron

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AUTHORS
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 Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15624448.
 Unpublished
 findPhrapList
 Direct Submission
 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
 as soon as it
be preserved
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 -- Genome Center
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Arabidopsis thaliana

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 COMMENT
 AUTHORS
TITLE
 JOURNAL
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 Direct Submitsion

Direct Submitsion

AL Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Lemcke@mips.biochem.mpg de, mayer@mips.biochem.mpg de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevanebbsrc.ac.uk

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be vlewed at: http://www.mips.biochem.mpg.de/proj/thai/ this fragment has an overlap with ATCHRIV51 at the 5' end and an overlap with ATCHRIV53 at the 3' end.

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(bases

Lemcke, K. a Unpublished

Pohl, T., Wei Unpublished

JOURNAL REFERENCE AUTHORS

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VERSION
KEYWORDS
SOURCE
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DEFINITION ACCESSION

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 Direct Submission
Direct Submission
Submitted (05-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 29, 2002 this sequence version replaced gi:14717253.
 Assembly p
 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
 be preserved
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Center code: BCM
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FEATURES

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AUTHORS
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JOURNAL

COMMENT

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Submitted (12-JUN-1997) Zoology,
Cromwell Rd, London SW7 5BD, UK
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A mitochondrial Hsp70 orthologue in Vairimorpha necatris
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Curr. Biol. 7 (12), 995-998 (1997)
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 Submitted (17-FEB-2000) Takahiko Hayakawa, Plantech Research Institute, Research Center; 1000 Kamoshida-cho, Aoba-ku, Yok Kanagawa 227-0033, Japan (E-mail:pri0012@cc.m-kagaku.co.jp, Tel:+81-45-963-3520, Fax:+81-45-962-7492)
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Hayakawa,T., Hamada,A. and Tanaka,A.
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 ABU38492 2637
Atriplex gmelini AgNHX1 mRNA
 Direct Submission
 21330247
 Isolation and characterization of a Na+/H+ antiporter gene from the halophyte Atriplex gmelini
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 recombinations with endogenous retroviral sequences and a cellular oncogene. The position of the oncogene junction was determined to be in the gag gene for pl0 at a position that removed the terminal 24 gag-encoded amino acids. The gag-onc fusion protein appears to be responsible for fibroblast and pre-B cell transformation. The authors call this oncogene y-cbl for Casitas B-lineage lymphoma.
 Draft entry and computer-readable sequence for [1] kindly submitted by W.Y.Langdon, 02-MAR-1989. Cas NS-1 is an acutely transforming murine retrovitus that induces pre-B and pro-B cell lymphomas. It was generated from the ecotropic Cas-Br-M virus by sequential
 J04169.1 GI:323269
gag:onc fusion protein; viral oncogene.
GAS NS-1 retrovirus DNA, isolated from me
previously infected with Cas-Br-M virus.
 Mouse Cas NS-1 retrovirus gag-onc fusion protein (v-cbl) gene, 3' end
 89145204
 v-cbl, an oncogene from a dual-recombinant murine retrovirus that induces early B-lineage lymphomas Proc. Natl. Acad. Sci. U.S.A. 86, 1168-1172 (1989)
 1 (bases 1 to 2711)
Langdon,W.Y., Hartley,J.W., Klinken,S.P., Ruscetti,S.K. and Morse,H.C. III.
 J04169
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analysis, using in preparation)

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 JOURNAL
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It may be
once, or 1
 Direct Submission
Submitted (28-JUN-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
 1 (bases 1 to 28990)
The C. elegans Sequencing Consortium.
The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
 Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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 U10414 28990 bp DNA linear INV Caenorhabditis elegans cosmid F42A10, complete sequence
 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemis or covered by high quality data (i.e., phred quality -30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence f more than one ml3 subclone.
 Direct Submission
Direct Submission
Submitted (05-CCT-2001) Department of Genetics, Washington
Submitted (05-CCT-3001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
 Direct Submission
Submitted (14-SEP-2001) Department of
University, Genome Sequencing Center,
 Direct Submission
Submitted (19-AUG-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
6 (bases 1 to 28990)
 Direct Submission
Submitted (06-JUN-1994)
University, 4444 Forest
5 (bases 1 to 28990)
 HTG.
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 University, Genome Se
Louis, MO 63110, USA
Submitted by:
 Waterston, R.
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 Unpublished
 Direct Submission
 The sequence of C. elegans
 Louis, MO
 Latreille, P
 99069613
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 (bases 1 to 28990)
 E: This sequence may not be the entire insert of this clone. y be shorter because we only sequence overlapping sections or longer because we provide a small overlap between
 Genome Sequencing Center
Department of Genetics, Wasi
St. Louis, MO 63110, USA,
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
 submissions
 rw@nematode.wustl.edu and jes@sanger.ac.uk
 Department of Genetics, Washington Park Avenue, St. Louis, MO 63108,
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 Washington
USA, and
 Genetics, Washington
4444 Forest Park Avenue,
 University
 by sequence from
 INV 05-OCT-2001
 USA
 chemistry
 all
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 USA
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 CDS
 CDS
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 CDS
 gene
 source
 The 5' cosmid is Y42G9A, 500 bp overlap; 3' cosmid is C23G10, 200 bp overlap. Actual start of this cosmid is at base position 7 of CELF42A10; actual end is at 7862 of CELC23G10.
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 /product="Hypothetical protein F42A10.4"
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/db_xref="GI:500737"
 yk406f4.5,
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yk74f7.3, yk74f7.5, yk112g6.3, yk112g6.5, yk158h11.
yk158h11.5, yk370c4.3, yk370c4.5, yk453c7.3, yk513d
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AUTHORS
TITLE
 FEATURES
 COMMENT
 REFERENCE
 SOURCE
 KEYWORDS
 VERSION
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 DEFINITION
 JOURNAL
MEDLINE
 AUTHORS
TITLE
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 ORGANISM
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CDS

Sg

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Seq_documentation_block:
LOCUS CEF11C1
 available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

This sequence is the entire insert of clone FIIC1. The start of this sequence (1. 104) overlaps with the end of sequence ALO23817. The end of this sequence (40749. .40852) overlaps with the start of
 Submitted (29-SEP-1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CBIO 15A, England and Department of Genetics, Washington University, St. Louis, Mo 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Sep 22, 1998 this sequence version replaced gi:1001858. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
 the specified clone. It may be shorter proverlapping sections once, or longer because overlap between neighbouring submissions.
 For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
 Palmer, S.
Direct Submission
 The C.elegans Sequencing Consortium 2 (bases 1 to 40852)
 Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
 Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
 Caenorhabditis elegans
 sequence AL008868.
 Caenorhabditis
 HTG; Denitrification;
 Z54270.1 GI:3642282
 name=F11C1
 IMPORTANT:
 (sites)
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 join(4336. .4463,5151. .5312,5860. .
6249. .6327,6386. .6513,6562. .6717,
7743. .7816,7965. .8229)
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 This sequence is NOT necessarily the entire insert of
 .40852
 It may be shorter because we only sequence once, or longer because we arrange for a sm
 Membrane glycoprotein;
 40852 bp שו
cosmid F11C1,
 DNA
 complete sequence.
 Caenorhabditis
 linear
 domain: PF01130 (CD36
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,6800. .6929,7378.
 Nuclear hormone
 INV 23-JAN-2002
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gene

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YVGQIKTNNGLTHLPWKYTEDTSDLRGTCDGTIQKFDIQKTDTVQFQSSFLCKKYNLH
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PKVVTESMVGIHPDFELHRPGTFYINPAGSTIGGEFRMMLSIPYFFGALLSAPHTYGA
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NAIMPSFTLTIGVWRNDYAWNYIIYNTYIIPNIVLGIGIGFTAVSLIAVILMGFCYFR
SKRNAKPFVLQOHRTBETWSVAE"
COMPLEMEDL()0in(8545. 8672,8990. 9065,9345. 9464,
9610. 9678))
 Join(13974 ...14034,14082 ...14311,14643 ...14753,14801 ...1496:
15119 ...15286,15367 ...15483,15531 ...16099,16524 ...16761,
16817 ...17259,17304 ...17403,17556 ...1772,17820 ...18049,
18103 ...18220,18332 ...18684,18898 ...19141,19185 ...19272,
19317 ...19386,19431 ...19557,19607 ...19765,19816 ...19996,
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 CDS
 35 GluLysArgGluThrLysGluLys 42
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gene

Length: 8
Gaps: 0
Percent Identity: 100.000

1 to:

SOURCE

VERSION

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AUTHORS
TITLE
 LOCUS AC090028
 REFERENCE
 KEYWORDS
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 DEFINITION
 ORGANISM
 JOURNAL
 AUTHORS
 Muzny, D. M., Adams, C., Adlo-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Biange, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen,
 Submitted (10-FFB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 23, 2001 this sequence version replaced gi:12739654.
 AC090028 50962 bp DNA linear HTG 16-OCT-2001 Homo sapiens chromosome 3q clone RP11-299G2, *** SEQUENCING IN PROGRESS ***, 48 unordered pieces.
 Unpublished
 AC090028.2 GI:14190614
 Direct Submission
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Weinstock,G. and Gibbs,R.
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Homo sapiens
 (bases
 (bases
 Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 99% of reads
Assembly program: Phrap; version 0.990329
 Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Assembly program: Phrap; version 0.990329 Consensus quality: 27482 bases at least Q40
 Center project name: HDET Center clone name: RP11-299G2
 Center code: BCM
 Center: Baylor College of Medicine
 HTGS_PHASE1.
 Submission
 1 to 50962)
 1 to 50962)
 -- Genome Center
 Summary Statistics
 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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COMMENT

TITLE

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* CONSISTS of 48 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
 Consensus quality: 35893 bases at least Q30 Consensus quality: 39768 bases at least Q20 Estimated insert size: 18665; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.2x in Q20 bases; sum-of-contigs estimation
 20866
20966
21681
21781
22810
22910
24085
 16269
16369
17151
17251
18073
 15069
15169
 14187
14287
 19869
 18969
 18869
 18173
 19969
 24084:
24184:
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contig
gap of
contig
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contig of 642 bp in length
gap of unknown length
contig of 636 bp in length
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contig
 gap of contig
 gap of contig
 gap of
 gap of
 gap of
 gap o
 conti
 gap o
 gap of
contig
 gap of unknown le
 gap o
 contig of 633 bp in length
 f unknown length
g of 1100 bp in length
if unknown length
g of 782 bp in length
of unknown length
 g of 643 bp in length
 of unknown lengt
lg of 651 bp in
 unknown le
of 696 bp
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of 675 bp
 of 1086 bp in length
unknown length
of 743 bp in length
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of 1029 bp in 1
unknown length
of 1175 bp in length
unknown length
of 928 bp in length
 of 715 bp in
 unknown le
of 897 bp
 unknown length of 900 bp in length
 of 822 bp
 unknown length
of 782 bp in le
 unknown length
of 804 bp in le
 unknown length
of 645 bp in length
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 unknown length of 667 bp in length
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of 683 bp in length
 of 638 bp
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 of 659 bp
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 of 647 bp in length
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bp in length
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Percent Similarity: 100.000
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HSDM723B3 APR 1.near PRI 04-APR-2001
Human DNA sequence from clone RP1-23B3 on chromosome 6q13-15
Contains the gene for a putative secreted protein ZSIG13, ESTs and
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lg of 792 bp in length
of unknown length
lg of 841 bp in length
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 ţo:
 4766 others
 REFERENCE
AUTHORS
TITLE
JOURNAL
 COMMENT
 FEATURES
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 requests: clonerequestesanger.ac.uk
On Oct 17, 2000 this sequence version replaced gi:10732514.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
 IMPORTANT: This sequence is not the entire insert of clone RP1-223E3 IT may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-223E3 is at 1 in this sequence. true left end of clone RP1-220N9 is at 59522 in this sequence. Location/Qualifiers
 http://www.sanger.ac.uk/HGP/Chr6
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPI-22B3 is from the sementary RPCI-1 constructed by the group of Pieter de Jong. For further details see
 Submitted (13-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
 Homo sapiens
 http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
 Direct Submission
 Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1329. .1552
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repeat: matches
 repeat: matches
 matches 7306.
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.289 of consensus
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The

ACCESSION VERSION KEYWORDS SOURCE

HTG

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seq\_name: gb\_pr:HSDJ223E3

DEFINITION

alignment\_scores: Quality: Ratio:

BASE COUNT ORIGIN

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FEATURES

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6331. .6391
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 8452. 8758 - Treat: matches 168. .188 of consensus /note="Aludo repeat: matches 1. .301 of consensus" 8759. .8910
 5046. .5435

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/note="AluSx repeat: matches 12. .296 of consensus"
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 e="L1MC2 repeat: matches 4362.
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 repeat: matches 1046. .1111 of
 matches 5189. .5826 of consensus
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Gaps:
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 54098
 from:
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 : 8
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| 7.00                                    |                 |                                        |                                       |            |
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| use<br>Programmer<br>Programmer         |                 |                                        |                                       |            |
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| #                                       | ea <sub>5</sub> |                                        |                                       |            |
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|                                         | <b>(A)</b>      | • • • • • • • • • • • • • • • • • • •  |                                       |            |
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Command line parameters:

-MODEL-frame+_D2n.model -DEV-xlh
-Q-/cgn2_1/USPTO_spoal/US08973363/runat_01082002_080123_19849/app_query.fasta_1.638
-Q-/cgn2_1/USPTO_spoal/US08973363/runat_01082002_080123_19849/app_query.fasta_1.638
-DB-M_Geneseq_033802_-OPMT-fastap_-SUFFIX-011p2n.rng
-GAPOP-4.500 -GAPOEXT-0.050 -MINMATCH-0.100 -LOOPECI-0.000
-LOOPEXT-0.000 -GGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-60.000
-XGAPEXT-60.000 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000
-YGAPEXT-60.000 -DELOP-6.000 -DELXP-7.000 -START=1
-MATRIX-01190 -TRANS-human40.cd1 -LIST=45 -DOCALIGN-200
-THR_SCORE-quality -THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -HEAPESIZE-500 -MXLLEN-0-MXLEN-200000000
-USER-US08973363_@CGN1_1_186 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARKIN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
 Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 521.050000
 About: Results were produced by the GenCore
Copyright (c) 1993-2000 Compugen Ltd
 WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.
 Search information block:
Query: US-08-973-363-14
 of: US-08-973-363-14 to: N_Geneseq_032802:*
 length:
 software, version 4.5.
 out_format : pfs
 .000
 0 143.39
0 129.24
0 130.46
0 139.24
127.85
124.42
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 7 143.81
148.10
148.10
9 161.09
9 167.02
195.57
9 256.60
9 265.66
9 265.66
9 275.86
9 297.88
9 300.55
9 336.15
9 336.15
9 336.15
9 336.15
9 336.15
9 336.15
9 336.15
9 336.15
 64.20
4 67.72
4 75.10
89.79
97.51
111.27
139.14
139.32
 4.6e-2
0.0043
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Ratio:
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from: 1

6 137

17

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Percent Identity:

97

46 1 . 826

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 A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CCl4 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-lA clones (see also AAT42752).
 Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
 Disclosure; Fig 7; 76pp; English.
 sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the W chromosome; ss.
 Location/Qualifiers
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/note= "base 52 disrupts the rithe translated amino arin Fig 7"
 motif.
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 G; 18
 T; 0 other;
 reading frame acid sequence
 for
given
 ín
 115.
115.
115.
115.
113.
110.
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.03
.92
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455
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459
464
787
806
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XX AAR42752;
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XX Bird; sex determinat;
XX Bird; sex determinat;
XX CHD-W; chromodomain-1
XX Gallus sp.
XX Gallus sp.
XX FH Key Locat
FT misc_difference 52
FT /*ta;
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PN W09639505-A1.
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YX D5-JUN-1996; 95GB-
XX O5-JUN-1995; 95GB-
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XX D12-DEC-19
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 complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
 101
 Disclosure; Fig 7; 76pp; English.
 Chicken CHD-1A insert motif
 AAT42752 standard; cDNA; 265
 34
 51
 17
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 ysGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAla
 1997-043127/04.
 chromodomain-helicase-DNA binding genes determine sex in used for sex determn, and to control sex of progeny
 sex determination;
 Quality:
Ratio:
 sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the \mathbf W chromosome; ss.
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 in Fig 7"
 Percent Identity:
 Ç
 ВP
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 30
 Length:
 T; 0
 136
 45
 : 11
: 0
: 100.000
 other;
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ω
 50
 6
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 Align seg 1/1
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14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
18 - AUG - 2000;
22 - AUG - 2000;
 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
 Human; secreted extracellular matrix protein; ss; immunomodu
Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant
cerebroprotective; thrombolytic; antimicrobial; ophthalmic;
antialzheimers; immune/autoimmune disease; HIV infection; ar
 30-JUN-2000;
07-JUL-2000;
 16-MAR-2000;
17-MAR-2000;
 cardiac arrest; tachycardia; angina; infection; corneal infections;
wound healing; immunogen; gene therapy; antisense; food additive.
 Human cDNA encoding a novel extracellular matrix protein, Seq ID No 153
 104
 26-JUL-2000;
14-AUG-2000;
 07-JUL-2000;
 07-JUN-2000;
 02-AUG-2001
 Homo sapiens.
 Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 cancers; hyperproliferative disorder; breast neoplasm; melanoma;
 human immunodeficiency virus; rheumatoid arthritis; multiple
 04-DEC-2001
 AAS31339
 14-AUG-2000;
14-AUG-2000;
 14-JUL-2000;
 28-JUN-2000;
 18-APR-2000;
 17-JAN-2001;
 WO200155368-A1
 14-AUG-2000;
 19-MAY-2000;
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 GluLysArgGluThrLysGluLysGluAsnLys 45
 standard; cDNA;
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о:
 2000US-0218290.
2000US-0220963.
2000US-0220964.
2000US-0224519.
2000US-0224519.
2000US-0225213.
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2000US-0225267.
2000US-0225268.
2000US-0225276.
2000US-0225447.
2000US-0225757.
2000US-0225759.
2000US-0225758.
2000US-0225759.
2000US-0225759.
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2000US-0217487.
2000US-0217496.
 (first entry)
 2000US-0215135
2000US-0216647
 2001WO-US01348
 2000US-0209467
 2000US-0198123
2000US-0205515
 2000US-0179065
 2000US-0225214
 2000US-0214886
 2000US-0190076
 2000US-0189874
 2000US-0180628
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 from:
 ВP
 Н
 to:
 136
 265
 immunomodulatory;
 cardiant; vascular;
 anaemia;
 cytostatic;
 sclerosis;
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PR 01-SEP-2000; 2000US-022894,
PR 01-SEP-2000; 2000US-022944,
PR 01-SEP-2000; 2000US-022944,
PR 01-SEP-2000; 2000US-022944,
PR 01-SEP-2000; 2000US-023944,
PR 01-SEP-2000; 2000US-023943,
PR 06-SEP-2000; 2000US-023144,
PR 08-SEP-2000; 2000US-023196,
PR 14-SEP-2000; 2000US-023396,
PR 12-SEP-2000; 2000US-023396,
PR 12-SEP-2000; 2000US-023499,
PR 12-SEP-2000; 2000US-023499,
PR 22-SEP-2000; 2000US-02349,
PR 22-SEP-2000; 2000US
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alignment_scores:
Quality:
Ratio:
 The invention relates to isolated nucleic acid molecules encoding cover human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased conditions are pression of SPs by binding with the sex polynucleotide or a vector expressing them may be administered to down regulate expression. The polynucleotides can any also be used as DNA probes in diagnostic assays. The SPs may also be used as antiquens to produce antibodies and to identify modulators can an antagonists may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of the disorders include for example: immune/autoimmune diseases (e.g. HIV conditions and activity of the disorders include for example: immune/autoimmune diseases (e.g. HIV conditions) and activity of the disorders include for example: infections, anaemia, rhewnatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. cardiac and multiple sclerosis) cancers and hyperproliferative disorders (e.g. arrest, tachycardia and angina), infections caused by bacteria, viruses and fingl and ocular disorders (e.g. corneal infections). Other uses can fully and ocular disorders (e.g. corneal infections). Other uses and include wound healing, maintenance of organs before transplantation,
Percent Similarity:
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17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
 Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
 WPI; 20
P-PSDB;
 Rosen
 Claim
 (HUMA-) HUMAN GENOME SCI INC
 2001-465572/50.
DB; AAU19768.
 SEQ ID No 153; 577pp;
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Length:
Gaps:
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 SM;
 100.
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 WO200155314-A2
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2000US-0209461

2000US-02151860

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2000US-0224519

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2000US-022571

2000US-022571

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2000US-022571

2000US-02257

2000U
 2001WO-US01324
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 system
 disorder;
 DNA;
 entry)
 antigen
 2121
 from:
 tigen; gene therapy; cancer; ion; Hirschsprung's disease; Meckel's diverticulum; ds.
 ВP
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 sequence
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 IJ
 appendicitis; chronic colitis;
 NO:
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08-DEC-2000
 1368 GAAAAAAGGGAAACGAAAGAGAAA 1391
 The present invention provides the protein and coding sequences of number of human digestive system antigens. These can be used in this diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
 Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
Homo sapiens
 Human; 5' EST; expressed sequence tag; secreted protein;
gene therapy; chromosome mapping; ss.
 Human secreted
 06-OCT-2000
 Disclosure; SEQ ID NO 2962; 986pp; English.
 Sequence 2121 BP; 906 A; 306 C; 407 G; 502 T; 0 other;
 WPI; 2001-502630/55.
 Rosen CA,
 (HUMA-) HUMAN GENÔME SCI INC
 35 GluLysArgGluThrLysGluLys 42
 Ratio:
 Barash SC,
 2000US-0249244.
2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249265.
 (first entry)
 protein 5' EST, SEQ ID NO: 29917.
 1.000
 from: 1
 Length: 8
Gaps: 0
Percent Identity: 100.000
 ВP
 SM;
 .
.
 2121
 cDNA isolation;
 colitis or
 of
the
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alignment_block:
US-08-973-363-14 x AAC25842
 seq_documentation_block:
ID AAK70025 standard; DNA; 312 BP
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK70025
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 Align seg 1/1 to: AAC25842 from:
 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
 The present sequence is one of a large number of 5′ ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5′ ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3′ untranslated region (UTR) of the mRNAs because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5′ ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5′ UTR is rarely included. 5′ ESTs are derived from mRNAs with intact 5′ ends and can therefore be used to obtain full length cDNAs with intact 5′ ends and can therefore be used to obtain full length cDNAs with intact 5′ ends and can therefore be a used to obtain upstream regulatory sequences and to design expression and secretion vectors.
 170 ATAAAGAAAGAAGCTGGTGAA 190
 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
 WPI;
 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
 Claim 1; SEQ ID 29917; 71pp + CD-ROM; English
WO200157182-A2
 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24837
 06-NOV-2001
 Sequence 294 BP; 96 A; 51 C; 72 G; 75 T; 0 other;
 Dumas Milne Edwards J,
 26-FEB-1999;
 21-FEB-2000; 2000EP-0200610.
 06-SEP-2000
 EP1033401-A2
 expression and secretion
 (GEST) GENSET
 29 IleLysLysGluAlaGlyGlu 35
 2000-500381/45
 (first entry)
 99US-0122487
 Duclert A, Giordano
 Length: 7
Gaps: 0
Percent Identity: 100.000
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6
 294
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24-FEB-2000
24-FEB-2000
117-MAR-2000
117-MAR-2000
119-MAY-2000
28-JUN-2000
29-JUN-2000
20-JUN-2000
20-JUL-2000
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11-AUG-2000
11-SEP-2000
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2000US-0211680
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2000US-0211680
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2000US-0218291
2000US-0218211
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2000US-0218211
2000US-021821
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2000US-021821
2000US-0218291
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2000US-0218240
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2000US-0218240
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2000US-0218484
2000US-02188364
2000US-02344981
2000US-02348363
2000US-02358364
2000US-02358364
2000US-02363681
 2001WO-US01354
 29-SEP-2000
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02-OCT-2000
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03-OCT-2000
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03-OCT-2000
03-OCT-2000
03-NOV-2000
03-DEC-2000
03-DEC
 Nucleic
 2001-483426/52
 acids
 HUMAN
 Barash
 2000US-0236370.
2000US-0237037
2000US-0237037
2000US-0237039
2000US-0237040
2000US-0237040
2000US-0241785.
2000US-0241808.
2000US-0241808.
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2000US-0246477.
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2000US-0246528.
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2000US-0246528.
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2000US-0249218.
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2000US-0249218.
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2000US-0249218.
2000US-02511856.
2000US-02511868.
2000US-02511868.
2000US-02511989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
encoding human
 GENOME
 SC,
 SCI
 Ruben
immune/hematopoietic antigen polypeptides,
 MS
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useful for preventing, diagnosing and/or treating cancers and

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seq_documentation_block:
ID AAS39061 standard; cDNA; 350 BP
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAS39061
 alignment_block:
 alignment_scores
 amino acid sequences given in AAM82170 to AAM91221. (1) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (1) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For C example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) of CC polynucleotides may be used to produce the secreted (I), by inserting CC protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and concer metastases of haematopoietic-derived cells. AAK64703 CC sequences from the present invention. AAK34942 to AAK34950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
 Align seg 1/1 to: AAK70025 from: 1
 US-08-973-363-14 x AAK70025
 Percent Similarity: 100.000
 Williams LT, Escobedo J, Innis MA, Garcia PD, Sudo
Reinhard C, Randazzo E, Kennedy GC, Pot D, Kassam
Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, La
Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-
 09-MAR-2000; 2000US-0188609
 09-MAR-2001; 2001WO-US07787
 Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic;
 Novel human diagnostic and therapeutic gene #2119.
 17-DEC-2001 (first entry)
 AAS39061;
 Sequence 312 BP; 133 A; 40 C; 82 G; 57 T; 0 other;
 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 Disclosure; SEQ ID NO 24837; 3071pp + Sequence Listing; English.
 metastasis
WPI; 2001-530177/58
 WO200166753-A2
 (HYSE-) HYSEQ INC.
 (CHIR) CHIRON CORP.
 37 ArgGluThrLysGluLysGlu 43
 50 AGGGAGACCAAGGAGAAGGAG 70
 Quality:
 Ratio:
 1.000
 Percent Identity: 100.000
 .
6
 Length:
 Drmanac S, Labat I;
ss WL, Stache-Crain B;
 Sudduth-Klinger J; ssam A, Lamson G;
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alignment_block:
US~08-973-363-14 x AAS39061/rev
 seq_documentation_block:
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 alignment_scores:
 Align seg 1/1 to reverse of: AAS39061
 Percent Similarity: 100.000
 The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to Inhibit tumour growth by modulating expression of a gene product. AAS35943 represent novel human diagnostic and therapeutic coding sequences of the invention.
The present invention describes a method for monitoring differential
 Claim 86; Page 1400; 3161pp; English.
 Monitoring differential expression of genes in filamentous uses fluorescence-labeled nucleic acids isolated from the c substrate of expressed sequence tags - \,
 Fusarium venenatum.
 Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
 Fusarium venenatum EST SEQ ID NO:2805.
 13-MAR-2001 (first entry)
 AAF10282 standard; cDNA; 427 BP
 260 AAAGAAGCAGGCGAGAAGAGA 240
 Sequence 350 BP; 53 A; 84 C; 60 G; 153 T; 0 other;
 Claim 1; Page 1126; 1193pp; English.
 Berka RM,
 22-MAR-1999;
 WO200056762-A2
 AAF10282
 WPI; 2000-594572/56.
 (NOVO) NOVO NORDISK BIOTECH INC.
 22-MAR-2000; 2000WO-US07781
 28-SEP-2000
 31 LysGluAlaGlyGluLysArg 37
 Quality:
Ratio:
 Rey MW, Shuster JR,
 99US-0273623.
 7.00
1.000
 Percent Identity: 100.000
 Kauppinen S,
 6
 Clausen IG,
 s fungal cells
cells and a
 Olsen PB;
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seq_documentation_block:
ID AAC00952 standard; cDNA; 468 BF
XX
AC AAC00952;
XX
DT 06-OCT-2000 (first entry)
XX
Human secreted protein 5' EST,
XX
Human; 5' EST; expressed sequen
KW Human; 5' EST; chromosome mappin
XX
Homo sapiens.
XX
PN EP1033401-A2.
XX
PN EP1033401-A2.
XX
PR 26-FEB-2000; 2000EP-0200610.
XX
PF 21-FEB-2000; 2000EP-020487.
XX
PF 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
 alignment_block:
 alignment_scores
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC00952
 CC expression of genes in a first filamentous fungal (FF) cell relative to CC expression of the same genes in one or more second filamentous fungal CC cells. The method uses filorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EET). The ESTS CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC discovered, possible functions of unknown open reading frames can be CC discovered, possible functions of unknown open reading frames can be CC discovered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC morphogenesis, recombination, metabolic or catabolic pathway CC engineering. Using ESTs provides several advantages over genomic or CC random cDNA clones including elimination of redundancy as one spot on an CC array equals one gene or open reading frame, and organisation of the CC microarrays based on function of the gene products to facilitate consists of the results. AAF11248 to AAF11247 represents ESTs from Aspergillus of CC AAF14879 to AAF1337 represents ESTs from Aspergillus oryzae; and CC AAF14879 to AAF1337 represents ESTs from Trichoderma reesei, which are CC all specifically claimed in the present invention.
 Percent Similarity:
 Align seg 1/1
 US-08-973-363-14 x AAF10282/rev
 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
 Sequence 427
 165 ACAAAAGAAAAGAAAACAAA 145
 ThrLysGluLysGluAsnLys 45
 Quality:
 Ratio:
 to reverse of: AAF10282
 вP;
 7.00
1.000
100.000
 120
 Α
 76
 Duclert
 EST,
 Percent
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 ВÞ
 97
 expressed sequence tag (5' EST) for
 SEQ ID
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 Gaps:
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 from:
 Giordano
 134 T; 0 other;
 NO: 950.
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; 100.000
 8
 from Aspergillus
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seq_documentation_block:
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 alignment_block:
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAC00953
 alignment_scores:
 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
 Align seg 1/1
 US-08-973-363-14 x AAC00952
 gene
 obtaining
 Human secreted
 often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where compare cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, contact the contact of the conta
 sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNA derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are
 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within t sequence. The 5' ESTs were prepared from total human RNAs or polyA+ R
 diagnostic,
 New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
 Dumas Milne Edwards J,
 21-FEB-2000; 2000EP-0200610
 06-SEP-2000
 EP1033401-A2
 Human;
 06-OCT-2000
 357
 obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
 (GEST) GENSET
 26-FEB-1999;
 Homo sapiens
 AAC00953
 Sequence 468
 upstream regulatory sequences and to design expression and secretion
 gene therapy and chromosome mapping procedures. They
 13 IleLysAlaGluLysGluAsn
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 therapy;
 2000-500381/45.
 5' EST;
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 SEQ ID
 to: AAC00952
 forensic,
 (first entry)
 BP;
 chromosome mapping;
 99US-0122487
 protein 5' EST,
 950;
 131 A;
 cDNA; 542 BP
 71pp + CD-ROM; English
 gene
 89 C; 116
 Duclert
 from:
 19
 377
 Percent Identity: 100.000
 therapy
 SEQ ID NO:
 ۳,
 Ą,
 tag;
 G; 131 T; 1 other;
 .
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 and
 Giordano
 468
 secreted protein; cDNA isolation;
 tag (5' EST) for to 5'ESTs and for
 mapping procedures
 are used to obtain
 within the polyA+ RNAs
 for
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Claim 1; SEQ ID 951; 71pp + CD-ROM; English

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 alignment_block:
US-08-973-363-14 x AAC00953
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Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
 seq_name:
 Align seg 1/1
 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An OFF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 Arabidopsis thaliana DNA fragment
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 13 IleLysAlaGluLysGluAsn 19
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 to:
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99US-0123180
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99US-0125788
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99US-0126785
99US-0128714
99US-0128714
99US-0128077
99US-0130077
99US-0130649
99US-0130691
99US-0130691
99US-0131449
99US-0131691
99US-0131691
 AAC00953
 151
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 from:
 451
 Length: 7
Gaps: 0
Percent Identity: 100.000
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 130
 SEQ ID NO: 78761.
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 04-MAY-1999
05-MAY-1999
06-MAY-1999
07-MAY-1999
07-MAY-1999
11-MAY-1999
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12-MAY-1999
12-MAY-1999
13-JUN-1999
13-JUN
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99US -0132485
99US -0132485
99US -0132485
99US -0132486
99US -0134219
99US -0134221
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 Align seg 1/1 to: AAC54696
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28-OCT-1999
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 Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 190
 Arabidopsis thaliana.
 Arabidopsis thaliana DNA fragment
 26
 GluileGlyileLysLysGlu
 (first entry)
 2000EP-0301439
 990S-0121825

990S-0123180

990S-0125788

990S-0126785

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990S-0126785

990S-012834

990S-0128945

990S-0130477

990S-0130477

990S-013049

990S-0130449

990S-0131448

990S-0132484

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99US-0160815.
99US-0160815.
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Gaps:
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| 27 JUL 1999 28 JUL 1999 28 JUL 1999 28 JUL 1999 28 JUL 1999 29 JUL 1999 20 AUG 1999 20 AUG 1999 20 AUG 1999 20 AUG 1999 21 AUG 1999 21 AUG 1999 21 AUG 1999 22 AUG 1999 23 AUG 1999 24 AUG 1999 25 AUG 1999 26 AUG 1999 27 AUG 1999 28 AUG 1999 29 AUG 1999 20 AUG 1999 21 AUG 1999 21 AUG 1999 22 AUG 1999 23 AUG 1999 24 SEP 1999 25 AUG 1999 27 AUG 1999 27 AUG 1999 28 SEP 1999 29 AUG 1999 21 AUG 1999 21 AUG 1999 21 AUG 1999 22 AUG 1999 23 AUG 1999 24 SEP 1999 25 AUG 1999 26 AUG 1999 27 AUG 1999 27 AUG 1999 28 SEP 1999 29 AUG 1999 21 AUG 1999 21 AUG 1999 21 AUG 1999 21 AUG 1999 22 AUG 1999 23 AUG 1999 24 SEP 1999 25 AUG 1999 26 AUG 1999 27 AUG 1999 28 SEP 1999 29 AUG 1999 21 AUG 1999 21 AUG 1999 22 AUG 1999 23 AUG 1999 24 AUG 1999 25 AUG 1999 26 AUG 1999 27 AUG 1999 28 AUG 1999 29 AUG 1999 21 AUG 1999 21 AUG 1999 22 AUG 1999 23 AUG 1999 24 AUG 1999 25 AUG 1999 26 AUG 1999 27 AUG 1999 28 AUG 1999 29 AUG 1999 21 AUG | 22-JUL-1999;<br>22-JUL-1999;<br>22-JUL-1999;<br>23-JUL-1999;<br>23-JUL-1999;<br>23-JUL-1999;<br>23-JUL-1999;<br>23-JUL-1999; |
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99US-0160770. 99US-0160814. 99US-0160815.

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26-OCT-1999
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 28-SEP-2000
 Aspergillus oryzae
 metabolic pathway engineering; catabolic pathway engineering; ss
 13-MAR-2001
The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative
 Monitoring differential expression of genes in filamentous fungal uses fluorescence-labeled nucleic acids isolated from the cells ausubstrate of expressed sequence tags -
 22-MAR-2000; 2000WO-US07781
 AAF11881 standard; cDNA;
 Claim 88; Page 1883-1884; 3161pp; English
 WPI; 2000-594572/56
 Berka RM,
 (NOVO) NOVO NORDISK BIOTECH INC (NOVO) NOVO NORDISK AS.
 22-MAR-1999;
 WO200056762-A2
 Multiple gene expression; filamentous fungal cell; EST;
 Aspergillus oryzae EST SEQ ID NO:4404
 28-OCT-1999
 26 GluIleGlyIleLysLysGlu
 GAGATTGGGATCAAAAAGGAG
 Rey
 (first entry)
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99US-0161360.
99US-0161361.
99US-0161361.
99US-0161920.
99US-0161993.
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: 1.000
: 100.000
 99US-0273623
 9908-0162142
 99US-0160981.
 99US-0160980.
 Shuster JR,
 710 BP
 from:
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 32
 Percent Identity:
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alignment_scores:
 Quality:
 seq_documentation_block:
ID AAI97871 standard; cDNA;
 alignment_block:
US-08-973-363-14 x AAF11881/rev
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI97871
 CC expression of the same genes in one or more second filamentous fungal CC cells. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTS CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC potential of the microorganisms to be improved. New genes may be CC discovered, possible functions of unknown open reading frames can be cidentified and gene copy number variation and stability can be consisted in culture conditions, environmental stress, spore consisted in culture several advantages over genomic or cardom cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the carray equals one function of the gene products to facilitate consists of the results. AAF07478 to AAF11247 represents ESTs from CC analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus organes; AAF11854 to AAF11878 represents ESTs from Trichoderma reesei, which are CC all specifically claimed in the present invention.
 Align seg 1/1 to reverse of: AAF11881
 Percent Similarity: 100.000
Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker
 AAI97871;
 233 AAAGAGGCGGGTGAAAAGAGG
 WPI; 2001-565584/63
 07-MAR-2000; 2000JP-0159195
 02-MAR-2001; 2001WO-JP01629
 13-SEP-2001.
 WO200166719-A1
 Homo sapiens.
 Human; neuroblastoma;
 Human neuroblastoma expressed polynucleotide SEQ ID NO 3946.
 13-NOV-2001
 Sequence
 (CHIB-) CHIBA PREFECTURE.
(HISM) HISAMITSU PHARM CO LTD
 31 LysGluAlaGlyGluLysArg
 710
 Ratio:
 BP;
 (first entry)
 7.00
1.000
 135 A;
 malignancy; cancer;
 195
 721
 213
 37
 Percent Identity: 100.000
 Ç
 ВP
 148 G; 231 T; 1 other;
 Length:
Gaps:
 from:
 tumour marker; N-myc;
 \vdash
 to:
 0 7
 from Aspergillus
llus oryzae; and
 TrkA;
 SS
```

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CC This polynucleotide sequence represents the DNA of the atRSp41 5'-UTR.
CC The invention relates to novel DNA sequences that function as promoters
CC of transcription of associated nucleotide sequences in plants. The
CC invention provides a DNA sequence capable of driving expression of an
CC associated nucleotide sequence, wherein said DNA sequence is obtainable
CC from genes of the atRSp (Arabidopsis thaliana arginine/serine-type plant
CC DNA molecules comprising an atRSp41 promoter, the invention also provides
CC expression vectors and transgenic plants comprising the promoters of the
CC invention. The DNA sequence of the invention is useful for expressing a
CC nucleotide sequence of interest. The nucleotide sequences proteins
CC for conferring a desirable phenotypic trait to a plant transformed with
CC the protein, where such traits include antibiotic resistance, virus
CC resistance, insect resistance, disease resistance, or resistance, virus
CC pests, herbicide tolerance, improved nutritional value, improved
CC performance in an industrial process or altered reproductive capability.
CC pests, herbicide tolerance, improved nutritional value, improved
CC performance in an industrial process or altered reproductive capability.
CC pests, herbicide tolerance, improved nutritional value, improved
CC pests, herbicide tolerance, improved nutritio
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alignment\_scores: 7.00
Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000

Length: 7
Gaps: 0
Percent Identity: 100.000

SXCCCCCXXXX

Claim 1; Page 2902; 2979pp; Japanese

for anti-cancer agents

The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.

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 Date: Aug 3, 2002 5:46
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 Results were produced by Copyright (c) 1993-2000 C
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 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 143
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Choi,D.W., Fenton Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
On Feb 22, 2001 this sequence version replaced gi:13109983.
 Hordeum vulgare
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; Triticeae; Hordeum.
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BG309136.2 GI:16313822
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//notes Nector: lambdaZAP; Site_1: EcoRI; Site_2: Xhol; /notes Nector: lambdaZAP; Site_1: EcoRI; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filtrer paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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6
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 911
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 Gene Collection (MGC)
 linear
 EST 21-FEB-2001
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 629
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GluLysArgGluThrLysGluLys 42
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 GGGGAAAAAAGAGAGACGAAAGAAAAG
 Quality:
 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
 Seq primer: puc 18 forward High quality sequence stop: 56.
 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
 Tel: +55-11-2704922
Fax: +55-11-2707001
 Contact: Simpson A.J.G.
 Proc. Natl. Acad. Sci. U.S.A.
 Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
 Nagai,M.A., da Silva,W. Jr., 2ago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens
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 (http://www.ludwig-org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-EN0092-
110101-006-d03_1&t3=2001-01-11&t4=1)
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1.000
100.000
 /note="Organ: lung_normal; Vector: puc18; Site_1: Smal; Site_2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
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51 c 31 g 78 t
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 EST 13-JUN-2001
 Briones, M.R.,
 Paulo-SP
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33 GAAAAAAGGGAAACGAAAGAGAAA 10

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AUTHORS
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 TITLE
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 16 GluLysGluAsnGluGluLysAsp 23
 BB416876 264 bp mRNA linear EST 16-JUL-
BB416876 RIKEN full-length enriched, 7 days embryo Mus musculus
CDNA clone C430048M07 3', mRNA sequence.
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consorti
 http://image.llnl.gov
Plate: LLAM9660 row: 1 column: 08
High quality sequence stop: 188.
 EST
 mRNA sequence.
BE787833
 601482830F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885463 5',
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 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 251)
 Homo sapiens
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 house mouse.
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 93
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Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carrinci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 264)

RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
R, P., Endo, T., Evkuda, S., Pukunishi, Y., Hara, A., Hayatsu, N.,
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Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, K., Shipagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Watanatsu, M., and Hayashizaki, Y.
 Quality:
Ratio:
 RIKEN MOUSE ESTS (KONDO).

Unpublished (2000)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
 further details
 Fax: 81-45-503-9216
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 45 a
 primer adapter of sequence [5'
GAGAGAGATTCTCGACTTAATTAATTCCCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and BamHI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
a 87 c 36 g 96 t
 contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGAACCATCATTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
 prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Percent Similarity: 100.000

US-08-973-363-14 x BB416876/rev

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 Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
 Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
 Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago truncatula
 MtBB32B09R1 MtBB Medicago truncatula cDNA clone MtBB32B09 T7, mRNA
 http://sequence.toulouse.inra.fr/Mtruncatula.html).
 nodules
 barrel medic
 AL377519.1 GI:9677271
 Medicago.
 (bases 1 to 269)
 ដ
 104 a
 reverse
 XhoI; Plants were grown in an aeroponic chamber on nitrogen-rich medium for 21 days. Three days before inoculation with Sinorhizobium meliloti, the medium was replaced by N-free medium. Root nodules (+ short adjacent root segments) were harvested 4 days post inoculation. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing CDNA inserts were
 mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

38 c 43 g 84 t
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 EST 03-AUG-2000
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 JOURNAL
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 source
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 31 LysGluAlaGlyGluLysArgGlu 38
 70
 17
AAGGAGGCAGGGGAGAAGCGAGAG
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tgzy24h01.rl 5', mRNA sequence.
N8260a
 Quality:
 Hehl,A., Manger,I., Marra,M., Sibley,L.D., Ajloka,J.A., Asl
Dietrich,N., Dubuque,T., Hilier,L., Kucaba,T., Man,K.L.,
Waterston,R.H. and Boothroyd,J.
Washb-Merck-Stanford-NIH Toxoplasma EST project
 Email: toxo@watson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further information
relating to organism, clone or library availability.
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Contact: Marra M
 Unpublished (1996)
 Toxoplasma gondii
Eukaryota; Alveelata; Apicomplexa; Coccidia; Eimeriida;
 EST
 N82699.1 GI:1258452
 WashU-Merck EST Project
 Sarcocystidae;
 Toxoplasma gondii.
 Ratio:
 (bases 1 to 295)
 primer: T3
 quality sequence stop: 283
 314 286 1800
314 286 1810
 85
 8.00
1.000
100.000
 Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was constructed by K.L. Wan, Cambridge University. CDNAs we synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."
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 from: 1
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38
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 to:
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 295
 269
 cDNA Toxoplasma gondii cDNA clone
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 EST 22-MAY-2000
 Aslett, M.A.
 cDNAs were
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 35 GluLysArgGluThrLysGluLys 42
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 1 (bases 1 to 303)
Zhao,B., Wang,X.M., Zhang,Q., Zhu,Z.M., Zhu,S.J. and Hui,R.T.
Cloning of Genes Responsible for Stroke
Unpublished (2000)
Contact: Bin Zhao
 AWDU/143 303 bp mRNA linear EST 01-JU EST00470 Plasmid Subtractive Library of Rat Cerebrum (stroke) Rattus norvegicus cDNA clone 3rdF2, mRNA sequence.
 Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6854
 Caenorhabditis elegans.
 Toward an expression map of the C.elegans genome Unpublished (1994) Contact: Yuji Kohara
Molecular Medical Center for Cardiovascular Disease
 Rattus norvegicus
 AW507143.1 GI:8133308
 Fax: 81-559-81-6855
 Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
 D71396.1 GI:1111103
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 ykohara@lab.nig.ac.jp.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases I to 315).
Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K., Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J., Hoffman,S.L. and Nussenzweig,V.
 315 bp mRNA linear EST 14-AUG-200: EST503096 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA clone PYCDX37, mRNA sequence.

BG604006
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
 Cardiovascular Institute, CAMS & PUMC 167, Bei Li Shi Lu, 100037, Beijing, P.R. China Tel: 86-10-68314466 ext 8136
 Exploring the transcriptome of the malaria sporozoite stage Proc. Natl. Acad. Sci. U. S. A. 98 (17), 9895-9900 (2001)
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Shanjun et al at 3rd Military Medical University Chongqing
, China. The Suppression Subtraction Hybridization (SSH)
was conducted at Fu Wai Hospital by Zhao Bin and Wang
was conducted at Fu China. Message RNA was extracted from
 Xianmei in Beijing, China. Message RNA was extracted from pooled whole cerebrum from stroke and control rats respectively. SSH had been conducted following manufacture's manual using 5ug mRNA. The SSH library was constructed by Zhao Bin and Wang Xianmei using pMD18-T vector. Randomly picked clones were sequenced at AB1-377 using MJ3R primer(AGCGGAPAACAATTTCACACAGG) by Wang Xianmei Zhao Bin and Zhang Qian."
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 Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
 Unpublished (1994)
Contact: Yuji Kohara
 Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 Email: gardner@tigr.org
Request for clones, please contact: Stefan Kappe,
kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
bepartment of Pathology New York University School of Medicine.
 EST
 D73021.1 GI:1112730
 Toward
 Tabara,H
 Caenorhabditis elegans.
 rel: 81-559-81-6854
Fax: 81-559-81-6855
 Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T.,
 Fax: 301 838 0208
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 134
 162
 ykohara@lab.nig.ac.jp.
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 Sugimoto, A. and
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AUTHORS
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 JOURNAL
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Class: sheared ends.
 9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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 DNA is from a doubled haploid provided by
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 Tom Osborn
 USA
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EST.
 CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lln1.gov/bbrp/lnage/thm1

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High quality sequence stop: 370.

Location/Qualifiers
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 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
The succession of the Cole, M.D., Michael R. Emmert-Buck, M.
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 Homo sapiens
 Unpublished (1997)
 Tumor Gene Index
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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 Location/Qualifiers
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CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.lnl.gov/bsrp/image/image.html
Seq primer: M13 Forward.
 Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Tratifutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buc
M.D., Ph.D.
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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 Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
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M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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source
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www-bio.llnl.gov/bbrp/image/image.html
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